

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2003, 20:03:04 ; Search time 13027 Seconds

(without alignments)
17854.427 Million cell updates/sec

Title: US-10-005-469-4

Perfect score: 7992

Sequence: 1 gccagcccccagatgggggc.....ctctctgcagatcaagtact (7992)

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl : *

1: gb_ba : *

2: gb_htg : *

3: gb_in : *

4: gb_om : *

5: gb_ov : *

6: gb_pat : *

7: gb_ph : *

8: gb_pl : *

9: gb_pr : *

10: gb_ro : *

11: gb_sts : *

12: gb_sy : *

13: gb_un : *

14: gb_vi : *

15: em_ba : *

16: em_fun : *

17: em_hum : *

18: em_in : *

19: em_mu : *

20: em_om : *

21: em_or : *

22: em_ov : *

23: em_pat : *

24: em_ph : *

25: em_pl : *

26: em_ro : *

27: em_sts : *

28: em_un : *

29: em_vi : *

30: em_htg_hum : *

31: em_htg_inv : *

32: em_htg_other : *

33: em_htg_mus : *

34: em_htg_pln : *

35: em_htg_rnd : *

36: em_htg_man : *

37: em_htg_vrt : *

38: em_sy : *

39: em_htgo_hum : *

40: em_htgo_mus : *

41: em_htgo_other : *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7982.6	99.9	7989	6 AX036255	AX036255 Sequence
2	7982.6	99.9	7989	12 SSR242652	AJ242652 Hepatitis
3	7960.6	99.6	8001	6 AX036254	AX036254 Sequence
4	7960.6	99.6	8001	12 SSR242654	AJ242654 Hepatitis
5	7943	99.4	8001	6 AX036259	AX036259 Sequence
6	7941.4	99.4	8001	6 AX036257	AX036257 Sequence
7	7935	99.3	8001	6 AX036261	AX036261 Sequence
8	7324.6	91.6	8637	6 AX036253	AX036253 Sequence
9	7324.6	91.6	8637	12 SSR242651	AJ242651 Hepatitis
10	7302.6	91.4	8649	6 AX036256	AX036256 Sequence
11	7302.6	91.4	8649	12 SSR242653	AJ242653 Hepatitis
12	7267.4	90.9	8639	6 AX472291	AX472291 Sequence
13	7266.4	90.9	8638	6 AX472314	AX472314 Sequence
14	7246.6	90.7	8638	6 AX472297	AX472297 Sequence
15	7245.6	90.7	8638	6 AX472315	AX472315 Sequence
16	7242	90.6	8642	6 AX472292	AX472292 Sequence
17	7239.2	90.6	8638	6 AX472296	AX472296 Sequence
18	7223.4	90.4	8648	6 AX472295	AX472295 Sequence
19	7219.4	90.3	8643	6 AX472294	AX472294 Sequence
20	6180.4	77.3	9605	14 HCJ238799	AJ238799 Hepatitis
21	6180.4	77.3	11076	6 AX036252	AX036252 Sequence
22	6162.8	77.1	11076	6 AX036260	AX036260 Sequence
23	6161.2	77.1	11076	6 AX036258	AX036258 Sequence
24	6154.8	77.0	11076	6 AX036262	AX036262 Sequence
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32	5386.6	67.4	9359	14 AF313916	AF313916 Hepatitis
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34	5372.8	67.2	9611	14 AY045702	AY045702 Hepatitis C
35	5362.4	67.1	9410	14 HPCX182	D50481 Hepatitis C
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42	5311.6	66.5	9379	14 AF207761	AF207761 Hepatitis
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45	5304	66.4	9373	14 AF208024	AF208024 Hepatitis

ALIGNMENTS

RESULT 1

AX036255

LOCUS AX036255

DEFINITION Sequence 4 from Patent EP1043393

ACCESSION AX036255

VERSION AX036255.1 GI:11225871

KEYWORDS

SOURCE

ORGANISM

Hepatitis C virus.

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Hepacivirus.

REFERENCE

1 (bases 1 to 7989)

AUTHORS Bartenschlager, R.D.

TITLE Hepatitis C virus cell culture system

JOURNAL Patent: EP 1043399-A 4 11-OCT-2000;

FEATURES		BARTENSCHLAGER RALF DR (DE)	
source		Location/Qualifiers	
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		/organism="Hepatitis C virus"	
		/db_xref="taxon:11103"	
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ORIGIN			
Query Match		99.9%;	Score 7982.6; DB 6; Length 7989;
Best Local Similarity		99.9%;	Pred. No. 0;
Matches 7985; Conservative		0;	Mismatches 4; Indels 0; Gaps 0;
QY	1	GCACACCCCGCATTTGGGGGGGACACCTCCACATATGATCTACCTCCCTGTGGAAGTACTG	60
DB	1	GCACACCCCGCATTTGGGGGGGACACCTCCACATATGATCTACCTCCCTGTGGAAGTACTG	60
QY	61	TCTTCAGCAGAAAGCGTCTAGCCATGAGCGTTAGTATGATGTGTGACGCTCCAGAGAC	120
DB	61	TCTTCAGCAGAAAGCGTCTAGCCATGAGCGTTAGTATGATGTGTGACGCTCCAGAGAC	120
QY	121	CCCCCCTCCGGAGAGCCATAGTGTGTGGGAACCGGTGAGTAAACCGGAATTGCGAG	180
DB	121	CCCCCCTCCGGAGAGCCATAGTGTGTGGGAACCGGTGAGTAAACCGGAATTGCGAG	180
QY	181	GACGACCGGGCTCTTTCTTGTGATCAACCCCGCTCAATGCTGAGAGATTTGGGCGCTGCC	240
DB	181	GACGACCGGGCTCTTTCTTGTGATCAACCCCGCTCAATGCTGAGAGATTTGGGCGCTGCC	240
QY	241	GCGAAGCTAGCTAGCGGAGTATGTTGGTGGCGAAAGGCGCTTGTGTACTGCTGATAGG	300
DB	241	GCGAAGCTAGCTAGCGGAGTATGTTGGTGGCGAAAGGCGCTTGTGTACTGCTGATAGG	300
QY	301	GTGCTTGGAGTGTGCCCCGGAGGCTGTGTAGACCGGTGACCATATGACGACCAATCTAAG	360
DB	301	GTGCTTGGAGTGTGCCCCGGAGGCTGTGTAGACCGGTGACCATATGACGACCAATCTAAG	360
QY	361	CTCAAAAGAAAAACCAAGGGGGCGCCCATGATTGAACAAGTGGATTTCAGCAGGTTCTC	420
DB	361	CTCAAAAGAAAAACCAAGGGGGCGCCCATGATTGAACAAGTGGATTTCAGCAGGTTCTC	420
QY	421	CGGCGCTTGGGTGAGAGGCTATTCGGCTATGACTGGGCAACAAGCAATCGGCTGCT	480
DB	421	CGGCGCTTGGGTGAGAGGCTATTCGGCTATGACTGGGCAACAAGCAATCGGCTGCT	480
QY	481	CTGATGCGCGGTGTTCGGGCTGTACAGGAGGGGGCGCCGGTTCTTTTGTCAAGACCG	540
DB	481	CTGATGCGCGGTGTTCGGGCTGTACAGGAGGGGGCGCCGGTTCTTTTGTCAAGACCG	540
QY	541	ACCTGTCCGGTGCCTGATGAACTGACGAGAGGAGGCGGCTATCGTGGCTGGCA	600
DB	541	ACCTGTCCGGTGCCTGATGAACTGACGAGAGGAGGCGGCTATCGTGGCTGGCA	600
QY	601	CGAGGGGGTTCCTTGGGCACTGTGCTCGACGTTGTCTGAAAGCGGGAAGGAGTGGC	660
DB	601	CGAGGGGGTTCCTTGGGCACTGTGCTCGACGTTGTCTGAAAGCGGGAAGGAGTGGC	660
QY	661	TGCTATTGGGCGAAGTGGCGGGGCGAGATCTCTGTATCTACCTTGTCTGCTGCGGAGA	720
DB	661	TGCTATTGGGCGAAGTGGCGGGGCGAGATCTCTGTATCTACCTTGTCTGCTGCGGAGA	720
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DB	721	AAGTATCATATGCTGATGCAATGCGCGGCTGATACGCTTGATCGGCTACCTGCC	780
QY	781	CATTGACACCAAGCAAGCAATGATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840
DB	781	CATTGACACCAAGCAAGCAATGATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840
QY	841	TTTGATATCAGATGATGTGAGCAAGAGATCAAGGGGCTGCGCCAGGCGGAAGTGTTC	900
DB	841	TTTGATATCAGATGATGTGAGCAAGAGATCAAGGGGCTGCGCCAGGCGGAAGTGTTC	900
QY	901	CGAGGCTCAAGGCGGCGCATGCCCGAGCGGAGGATCTGTGTGATACCATGGGATGCT	960
DB	901	CGAGGCTCAAGGCGGCGCATGCCCGAGCGGAGGATCTGTGTGATACCATGGGATGCT	960
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DB	961	GCTTGGCGAATATGATGATGGAATGAGCGGCTTTTCTGTGATTCAGTACGATGTGCGCGC	1020
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DB	1021	TGGGTGTGGGAGCGGCTATCAGAGATAGCGTGGCTACCGGTATGATGCTGAGAGAGC	1080
QY	1081	TTGGGCGGGAATGAGCTGACCGCTTCTGTGCTTTACGATATGCGCGCTCCGATTTGCG	1140
DB	1081	TTGGGCGGGAATGAGCTGACCGCTTCTGTGCTTTACGATATGCGCGCTCCGATTTGCG	1140
QY	1141	AGCGATGCGCTTCTATCGCTTCTTACAGAGTCTTCTGATTTAAGACAGCAGACAAG	1200
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DB	1201	GTTTCCCTCTAGCGGAGATCAATTCGCGCCCTCCCTCCCTCCCTTAAGTTACTGCG	1260
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DB	1261	CGAAGCGCTTGAATTAAGCGCGGTGTGCTGTCTATATGTTATTTTCACCATATTG	1320
QY	1321	CGGTCTTTTGGCAATGTGAGGGCGCGGAAACCTGACCTCTTCTTGAAGACATTTCT	1380
DB	1321	CGGTCTTTTGGCAATGTGAGGGCGCGGAAACCTGACCTCTTCTTGAAGACATTTCT	1380
QY	1381	AGGGTCTTTTCCCTCTGCGCAAGAGATGCAAGTCTGTGATGATCGTGAAGAGAGA	1440
DB	1381	AGGGTCTTTTCCCTCTGCGCAAGAGATGCAAGTCTGTGATGATCGTGAAGAGAGA	1440
QY	1441	GTTCTCTGSAAGCTTCTGTAAGACAACAACGCTGTAGCGAACCCTTTCAGAGCAGCG	1500
DB	1441	GTTCTCTGSAAGCTTCTGTAAGACAACAACGCTGTAGCGAACCCTTTCAGAGCAGCG	1500
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DB	1621	TGGCTCTCTCAAGGATATTCACAAAGGGGCTGAAGATGCCAGAGGATACCCATTGT	1680
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DB	1741	AACGCTAGGCGCCCGGAAACACGAGGAGCGTGTTCCTTTGAAAAACGATAATACC	1800
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DB	1801	ATGGGCGCTATTACGGCTACTCCCAACAGACGAGGCTACTTGGCTGCATCATACCT	1860
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DB	1861	AGCCTCACAGGCGGGGAGAGAACAGAGTGTGAGGAGGAGTGTGAGTGTCTCACCGCA	1920
QY	1921	ACACATCTTTCTGTGCGACCTGCGTCAATGGCTGTGTGAGTGTCTATCATGTGTGC	1980
DB	1921	ACACATCTTTCTGTGCGACCTGCGTCAATGGCTGTGTGAGTGTCTATCATGTGTGC	1980
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Db	4681	ACGGTGTGTAAGTGAATTTCAAGACCTGGTCCACGTCCAAAGCTCCTCCCGCAATTCGCGGA	4740
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QY	4801	CAAAACACCTGGCCCATGTGGAGCAGACAGATCACCGGACATGTGAAAAAGGTTTCATAGG	4860
Db	4801	CAAAACACCTGGCCCATGTGGAGCAGACAGATCACCGGACATGTGAAAAAGGTTTCATAGG	4860
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1. Lehmann, M., Korneier, F., Koch, J., Herian, U., Theilmann, L. and
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Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell
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PUBMED 10390360
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AUTHORS Bartenschlager, R.
TITLES Direct Submission
JOURNAL Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology,
Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67,
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ORGANISM Hepatitis C virus.
REFERENCE 1 (bases 1 to 8001)
AUTHORS Bartschlag, R.D.
TITLE Hepatitis C virus cell culture system

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QY 841 TGGAGCCGGGCTTGTGATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 841 TGGAGCCGGGCTTGTGATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900

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QY	889	CCGAACTGTTGGCAGAGCTCAAGGGCGGAGTACCAGGCGAGAGATCGTGTACCC	948
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QY	949	ATGGCATGCGTCTGTGGCGAATATCATGTGAGAAATAGCCGCTTTCTGTGATTCATC	1008
Db	961	ATGGCATGCGTCTGTGGCGAATATCATGTGAGAAATAGCCGCTTTCTGTGATTCATC	1020
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Db	1021	ACTGTGCGCGGTGGSSTGTGCGGAAACCGCTATACGACATAGCGTTGGCTTACCCGTATA	1080
QY	1069	TTGCTGAAGAGCTTGGCGGGCGAATGGGCGTAGCCGTTCTCTGTGCTTTAGAGTATGCGC	1128
Db	1081	TTGCTGAAGAGCTTGGCGGGCGAATGGGCGTAGCCGTTCTCTGTGCTTTAGAGTATGCGC	1140
QY	1129	CTCCGATTCGACAGCCATCGGCTTCTATGCGCTTCTTAGAGAGTCTTCTGAGTTTAAA	1188
Db	1141	CTCCGATTCGACAGCCATCGGCTTCTATGCGCTTCTTAGAGAGTCTTCTGAGTTTAAA	1200
QY	1189	CAGACCAACAGGTTTCCCTTAGGCGGATTCATTCGCGCCCTCTCCCTCCCGCCGCT	1248
Db	1201	CAGACCAACAGGTTTCCCTTAGGCGGATTCATTCGCGCCCTCTCCCTCCCGCCGCT	1260
QY	1249	AAGTTCCTGGCGAAGCGGTGGAATAGAGCCGGTGTGGTTTGCTATATGTATTT	1308
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QY	1309	TCCACCATATTCGCGTCTTTTGCAATGTGAGGGCCGGAACCTGCGCCCTGTCTTG	1368
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QY	1369	ACGAGCTTCCTTGGGGGTCTTTCCTCTCGCCAAAGAGATCAAGTCTTTGAATGTC	1428
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Db	1561	TAAATATACACCTGCAAGGGCGACACACCAGTGCACAGTGTAGTGAATGTTGTG	1620
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Db	1621	GAAGAAGTCAAAATGCTCTCTTAACCGTATTCACAAAGGGCTTAAGAGATGCCCAGAG	1680
QY	1669	GTACCCCATGTGTGGATGTGATCTGAGGGCCCTCGGTGTCACATGCTTTACATGTGTTAG	1728
Db	1681	GTACCCCATGTGTGGATGTGATCTGAGGGCCCTCGGTGTCACATGCTTTACATGTGTTAG	1740
QY	1729	TCGAGGTTAAAAACGCTTAGGCCCCCGAACACGAGGAGCGTGTTCCTTTGAAAAA	1788
Db	1741	TCGAGGTTAAAAACGCTTAGGCCCCCGAACACGAGGAGCGTGTTCCTTTGAAAAA	1800
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QY	1909	GTCGTCCACCGAACAACAATTTTCGTGGGAGACTGCGTAAAGGGGTGTGTGAGCTGTC	1968
Db	1921	GTCGTCCACCGAACAACAATTTTCGTGGGAGACTGCGTAAAGGGGTGTGTGAGCTGTC	1980
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Dp	2041	ACCAATGTGAGACAGACCTGTCGGCTGGCAGACGCCCCGGGGCGCTTCCTTGACA	2100
Qy	2089	CCATGCACCTGGGGAGAGCTCGGACCTTTACTTGGTACAGAGCATCGATTCATTCG	2148
Dp	2101	CCATGCACCTGGGGAGAGCTCGGACCTTTACTTGGTACAGAGCATCGATTCATTCG	2160
Qy	2149	GTCGCGCGCGGGAGAGACAGAGGGGGAGGACTTATCCGCCAGGCGCTTCCTACTTG	2208
Dp	2161	GTCGCGCGCGGGAGAGACAGAGGGGGAGGACTTATCCGCCAGGCGCTTCCTACTTG	2220
Qy	2209	AAGGCGCTTTCGGGGGCGTCACATGTCGTGCCCCTCGGGGAGCCTGTGGGACATCTTG	2268
Dp	2221	AAGGCGCTTTCGGGGGCGTCACATGTCGTGCCCCTCGGGGAGCCTGTGGGACATCTTG	2280
Qy	2269	GTCGCGGTGACACCGAGGGGTTTCGAGGCGGTGAGCTTTTATCCGTCGAGTATG	2328
Dp	2281	GTCGCGGTGACACCGAGGGGTTTCGAGGCGGTGAGCTTTTATCCGTCGAGTATG	2340
Qy	2329	GAAPCACATATGCGGTCCCCGGTCTTACGAGACACTGTCCTCCGCGCTACCGAG	2388
Dp	2341	GAAPCACATATGCGGTCCCCGGTCTTACGAGACACTGTCCTCCGCGCTACCGAG	2400
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Dp	2401	ACATTCAGGTGGCCCATCTACAGCCCCCTACTGTATGCGGGAAGACACTAAGTGGCG	2460
Qy	2449	GCTTCGTATGCAGCCCAAGGGATATAGGTGTTGTCTGAACCCGTGTCGCGCCGACCC	2508
Dp	2461	GCTTCGTATGCAGCCCAAGGGATATAGGTGTTGTCTGAACCCGTGTCGCGCCGACCC	2520
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Dp	2581	GTAGGACCATCATCACGCGGGTCCGCCATCACGACTCCACCTATGAGCAAGTTTCTGGC	2640
Qy	2629	GAGCGTGTGCTCTGTGGGGCGCCTATACATCATATATGTATGTATGGTCCACTCAAT	2688
Dp	2641	GAGCGTGTGCTCTGTGGGGCGCCTATACATCATATATGTATGTATGTATGGTCCACTCAAT	2700
Qy	2689	GACTCGACCACTATTCCTGGGACATCGGACATCTCTGGACCAAGCGGCTGGAGCG	2748
Dp	2701	GACTCGACCACTATTCCTGGGACATCGGACATCTCTGGACCAAGCGGCTGGAGCG	2760
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Dp	2761	CGAGCTGTGCTGCTGCCACCGGCTACGGCTCCGGGATCGTCACGCTGCCATCCAAAC	2820
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Dp	2821	ATCGAGAGGTGGCTGTGTCACAGCACTGAGAAATCCGCTTTATGGCAAGCATCCCC	2880
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Dp	2881	ATCGAGACCATCAAGGGGGAGGAGGAGCCTCATTTTCTGCATTTCCAGAAATGTGAT	2940
Qy	2929	GAGTCGCCCGCGAAGGTGTCGCCGCTCGGACATCATGCTGTAGCATATTTACGGGGCCTT	2988
Dp	2941	GAGTCGCCCGCGAAGGTGTCGCCGCTCGGACATCATGCTGTAGCATATTTACGGGGCCTT	3000
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Dp	3001	GATGTATCCCTCATACCACTATGCGGAGACGCTCATGTGCTAGGACAGGAGCCTCTAATG	3060
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DEFINITION	Hepatitis C virus replicon I389/NS3-3'UTR.		
ACCESSION	AJ242654		
VERSION	AJ242654.1		
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ORGANISM	Hepatitis C virus replicon I389/NS3-3'UTR.		
REFERENCE	1 (bases 1 to 8001).		
AUTHORS	Lothmann V., Koller F., Koch J., Herian U., Theilmann L. and Bartschlag R.		
TITLE	Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line		
JOURNAL	Journal of Virology		
REFERENCE	1993		
AUTHORS	Bartschlag R.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-MAY-1999) Bartschlag R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY		
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RESULT	5			
LOCUS	AX036259			
DEFINITION	Sequence 8 from Patent EP1043399.	8001 bp	DNA	linear
ACCESSION	AX036259			PAT 16-NOV-2000
VERSION	AX036259.1	GI:1125875		
KEYWORDS				
SOURCE	Hepatitis C virus.			
ORGANISM	Hepatitis C virus.			
	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;			
	Hepadnavirus.			
REFERENCE	1 (bases 1 to 8001)			

AUTHORS Bartenschlager R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patient: BP 1043399-A 8 11-OCT-2000;
BARTENSCHLAGER RAUF DR (DE)
FEATURES Location/Qualifiers
Source 1. 8001
/organism="Hepatitis C virus"
/db_xref="taxon:11103"

BASE COUNT 1650 a 2369 c 2247 g 1735 t
ORIGIN

Query Match 99.4%; Score 7943; DB 6; Length 8001;
Best Local Similarly 99.7%; Pred. No. 0;
Matches 7974; Conservative 0; Mismatches 15; Indels 12; Gaps 1;

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Db 1 GCCAGCCCCGATGGGGGGGAGACATCCACCATAGATCACTCCCTGTGAGAACTACTG 60
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Db 121 CCCCCCTCCCGGAGAGCATAGTGTCTGGAGACCGGTGATACACCGGAATTGGCAG 180
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Dd	3661	ACCAATATCATATAGGATGATGTGCGCTGACCTGGAGTGTCTACAGAGACCTGGGTG	3720
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ORGANISM Hepatitis C virus.
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AUTHORS Bartenschlager, R.D.
TITLE Hepatitis C virus cell culture system
JOURNAL Patent: EP 1043399-A 6 11-OCT-2000;
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ACCESSION	AX036261			
VERSION	AX036261.1	GI:11225877		
KEYWORDS	Hepatitis C virus. Hepatitis C virus viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepadnavirus.			
SOURCE				
ORGANISM				
REFERENCE	1 (bases 1 to 8001)			
AUTHORS	Bartenschlager R.D			
TITLE	Hepatitis C virus cell culture system			
JOURNAL	Patent: EP 1043399-A 10 11-OCT-2000;			
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ORIGIN				
Query Match	99.3% Score 7935; DB 6; Length 8001:			
Best Local Similarity	99.6%; Pred. No. 0;			
Matches 7969; Conservative	0; Mismatches 20; Indels 12; Gaps 14			
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Dd	181	GACGACCGGGTCTTCTTTGTGATCAACCCGCTCAAATGCTTGAGATTTGGGCGTGGCCCC 240		
QY	241	GCGAGACGTGAGCCGAGTGTGTTGGGTGCGGAAGACCTTGTGGTACTGACCTGATAG 300		
Dd	241	GCGAGACGTGAGCCGAGTGTGTTGGGTGCGGAAGACCTTGTGGTACTGACCTGATAG 300		
QY	301	GTCGTTGCGAGTGGCCCCGGAGGCTCTGTAGACCGCTGCACATGACACGAAATCTTAAC 360		
Dd	301	GTCGTTGCGAGTGGCCCCGGAGGCTCTGTAGACCGCTGCACATGACACGAAATCTTAAC 360		
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D	421	ACGAGGTTTCGGCGCGCTTGGGTGGAAAGCTATTGGGCTATACGTGGGCACAACGA	480
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D	541	TGTTCAGAACCCGACCTGTCCGGTGGCCCTAATGAACGTGAGGACCAAGGCGGCGCAT	600
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D	721	CTCTGGCGAAGAAAGTATCCATCATGGCTGATGCAATGGCGGCGGTGATACGCTTGATC	780
Q	769	CGGCTACCTGCCATTTGACACCACCAAGCAAAATGTGCTGACGAGAGCACTACTCGGA	828
D	781	CGGCTACCTGCCATTTGACACCACCAAGCAAAATGTGCTGACGAGACACTACTCGGA	840
Q	829	TGGAAGCGGCTTGTGATCAGAGATGTGGACCAAGACATCAGGGGCTCGCGCAG	888
D	841	TGGAAGCGGCTTGTGATCAGAGATGTGGACCAAGACATCAGGGGCTCGCGCAG	900
Q	889	CCGAACGTTCGGCAGGCTAAGGCGCGCATGCCCAAGGCGAGGATCTCGTCGTGACCC	948
D	901	CCGAACGTTCGGCAGGCTAAGGCGCGCATGCCCAAGGCGAGGATCTCGTCGTGACCC	960
Q	949	ATGGGATGCTCTGCTCCGATATCATGTGTGAAATGACCGCTTTTCTGATTCATCG	1008
D	961	ATGGGATGCTCTGCTCCGATATCATGTGTGAAATGACCGCTTTTCTGATTCATCG	1020
Q	1009	ACTGTGCGGCGCTGGGTGTGGCGGACCGGCTATAGAGCATAGGCTTGACCGGATGA	1066
D	1021	ACTGTGCGGCGCTGGGTGTGGCGGACCGGCTATAGAGCATAGGCTTGACCGGATGA	1080
Q	1069	TTCGTAAGAGCTTGGGCGGCAATGAGGCTTACCGCTTCCTGCTTACGGTATCGCG	1126
D	1081	TTCGTAAGAGCTTGGGCGGCAATGAGGCTTACCGCTTCCTGCTTACGGTATCGCG	1140
Q	1129	CTCCGATTCGACGCGATGCCCTTATAGGCTTCTTGACGAGTCTCTAGATTAA	1188
D	1141	CTCCGATTCGACGCGATGCCCTTATAGGCTTCTTGACGAGTCTCTAGATTAA	1200
Q	1189	CAGACCAACAGGTTTCCTCTTACGGGATCAATTCGCGCCCTCTCCCTCCCGCCCT	1248
D	1201	CAGACCAACAGGTTTCCTCTTACGGGATCAATTCGCGCCCTCTCCCTCCCGCCCT	1260
Q	1249	AACGTTACTGGCCGAAGCGCTTGGATTAAGCGCGGTGTCCGTTGCTATATGTAATT	1308
D	1261	AACGTTACTGGCCGAAGCGCTTGGATTAAGCGCGGTGTCCGTTGCTATATGTAATT	1320
Q	1309	TCCACCATATTGCCGCTTTTGGCAATGTAGGGCCCGGAACCTGACCTGTCTTCTG	1366
D	1321	TCCACCATATTGCCGCTTTTGGCAATGTAGGGCCCGGAACCTGACCTGTCTTCTG	1380
Q	1369	ACGACCATTTCTAAGGCGCTTCCCGCTCGCCAAAGAGATGCAAGGCTGTGGAATGC	1426
D	1381	ACGACCATTTCTAAGGCGCTTCCCGCTCGCCAAAGAGATGCAAGGCTGTGGAATGC	1440
Q	1429	GTTGAAGAGAGCATTTCTCTGGAAGCTTTTGAAGACAAACGTCGTGACGACCTT	1486

Db	1441	GTGAGGAGACAGCTGTCTCTCGAAGGCTCTTTGAACACAAACAAGCTCTGTAGGACCTT	1500
Qy	1489	TGCAGGACGCGAACCCTCCACTGTGGCAGCAGGTGCTCTGTGGCCAAAGACCACTGTGA	1548
Db	1501	TGCAGGACGCGAACCCTCCACTGTGGCAGCAGGTGCTCTGTGGCCAAAGACCACTGTGA	1560
Qy	1549	TAAATACACTGTGGAAGGGGAGCACAACCCAGTCGACAGTGTGATGTGATAGTGTG	1608
Db	1551	TAAATACACTGTGGAAGGGGAGCACAACCCAGTCGACAGTGTGATGTGATAGTGTG	1620
Qy	1609	GAAGAGTCAATGCTCTCTCTCAGCGTATTCACACAGGGGCTGAAAGATGCCAGAG	1668
Db	1621	GAAGAGTCAATGCTCTCTCTCAGCGTATTCACACAGGGGCTGAAAGATGCCAGAG	1680
Qy	1669	GTACCCCATGTATGGGATGTGATCTGATGAGGGGCTCGGTGCACATGCTTACATGTTAG	1728
Db	1681	GTACCCCATGTATGGGATGTGATCTGATGAGGGGCTCGGTGCACATGCTTACATGTTAG	1740
Qy	1729	TCGAGGTAAAAACGCTGTAGGGCCCCCGACACACGGGAGCTGGTTTCTTTGAAAAA	1788
Db	1741	TCGAGGTAAAAACGCTGTAGGGCCCCCGACACACGGGAGCTGGTTTCTTTGAAAAA	1800
Qy	1789	CACGATATATACCATGCGGCTATTACGGCTACTCCCAACACCGGAGGCTACTTGGC	1848
Db	1801	CACGATATATACCATGCGGCTATTACGGCTACTCCCAACACCGGAGGCTACTTGGC	1860
Qy	1849	TGCATCATCACTATACCTTCACAGGCGGGAGAGCAACAGTGGAGGGGAGGTCCAGGTG	1908
Db	1861	TGCATCATCACTATACCTTCACAGGCGGGAGAGCAACAGTGGAGGGGAGGTCCAAAGTG	1920
Qy	1909	GTCCTCACCGCACACATCTTTCTCTGAGGACTGCTGTCAATGCGCTGTGTTGACGTG	1968
Db	1921	GTCCTCACCGCACACATCTTTCTCTGAGGACTGCTGTCAATGCGGTGTGTTGACGTG	1980
Qy	1969	TATCATGCTGCGGCTCAAAAGACCTTGCGCGGCCCAAGAGGGCCATACCCAAATGTAC	2028
Db	1981	TATCATGCTGCGGCTCAAAAGACCTTGCGCGGCCCAAGAGGGCCATACCCAAATGTAC	2040
Qy	2029	ACCAATGTGACACGAGACTGTGTGGCTGSCAAAGCCCCCGGGGGCGCTTCTTGACA	2088
Db	2041	ACCAATGTGACACGAGACTGTGTGGCTGSCAAAGCCCCCGGGGGCGCTTCTTGACA	2100
Qy	2089	CCATCCACTCGGGAGCTGSGGACCTTATTTGTCACGAGGATGCGCATGCTATTCG	2148
Db	2101	CCATCCACTCGGGAGCTGSGGACCTTATTTGTCACGAGGATGCGCATGCTATTCG	2160
Qy	2149	GTGGCCGCGGGGCGAGCAGCAGGGGAGGCTACTCTCCCGCAGGCCGCTCTACTTG	2208
Db	2161	GTGGCCGCGGGGCGAGCAGCAGGGGAGGCTACTCTCCCGCAGGCCGCTCTACTTG	2220
Qy	2209	AAGGCTCTTGGGGGCTGTCACTCTCTGCCCCCGGGAGACGTGTGGGCACTTTTGG	2268
Db	2221	AAGGCTCTTGGGGGCTGTCACTCTCTGCCCCCGGGAGACGTGTGGGCACTTTTGG	2280
Qy	2269	GTGGCCGCTGACCCAGCGGGGTTGCAAGGCGGTGATGATTTGTACCGTGAAGTCTAG	2328
Db	2281	GTGGCCGCTGACCCAGCGGGGTTGCAAGGCGGTGATGATTTGTACCGTGAAGTCTAG	2340
Qy	2329	GAAACACTATGCGGTCCCGGCTTTACAGGACACATCTGCTCCCTCGGGCCGTACCGAG	2388
Db	2341	GAAACACTATGCGGTCCCGGCTTTACAGGACACATCTGCTCCCTCGGGCCGTACCGAG	2400
Qy	2389	ACATTCACAGTGGCCATCTACAGGCCCTACTGTAGCGGCAAGAGCACTAAGGTGCG	2448
Db	2401	ACATTCACAGTGGCCATCTACAGGCCCTACTGTAGCGGCAAGAGCACTAAGGTGCG	2460
Qy	2449	GCTGCGTATGACCCCAAGGCTATAGGTGCTTGTCTGAACCCGTCGTCGCCGCCAC	2508
Db	2461	GCTGCGTATGACCCCAAGGCTATAGGTGCTTGTCTGAACCCGTCGTCGCCGCCAC	2520
Qy	2509	CATAGTTTCGGGGCTATATGTCAAGCAGATGTTGCAACCTTAACATCGAAGCCGG	2568
Db	2521	CATAGTTTCGGGGCTATATGTCTTAAGCAGATATGTTGCAACCTTAACATCGAAGCCGG	2580

QY	2569	GTAGGACCACTACACACAGGGGTGGCCCATCAGTACTCCACTATGACAGATTCTTGCC	2628
Db	2581	GTAGGACCACTACACACAGGGGTGGCCCATCAGTACTCCACTATGACAGATTCTTGCC	2640
QY	2629	GACGGTGGTGTCTGTGGGGCGCTTATGACATCATATATGTGATGAGTGCCTCACT	2688
Db	2641	GACGGTGGTGTCTGTGGGGCGCTTATGACATCATATATGTGATGAGTGTGCCTCACT	2700
QY	2689	GACTGCAGCACTATTCCTGGGCAATCGGCAACAGTCTGGACACAGCGGAGCGGTGGAGCG	2748
Db	2701	GACTGCAGCACTATTCCTGGGCAATCGGCAACAGTCTGGACACAGCGGAGCGGTGGAGCG	2760
QY	2749	CGACTCGTGTGTCTGCGCACCCGTACGCTCCGGGATGGGTGACGTGCTGCATATCCAAAC	2808
Db	2761	CGACTCGTGTGTCTGCGCACCCGTACGCTCCGGGATGGGTGACGTGCTGCATATCCAAAC	2820
QY	2809	ATCAGAGAGGTGGCTGTCTGTCCACACTGAGAAATCCCTTTATATGCGCAAGCCATCCCC	2868
Db	2821	ATCAGAGAGGTGGCTGTCTGTCCACACTGAGAAATCCCTTTATATGCGCAAGCCATCCCC	2880
QY	2869	ATCAGAGCACTAAGGGGGGGGAGGCAACCTATTTCTGTGCATATCCAAAGAAATGTGAT	2928
Db	2881	ATCAGAGCACTAAGGGGGGGGAGGCAACCTATTTCTGTGCATATCCAAAGAAATGTGAT	2940
QY	2929	GAGCTCGCCGGGAGAGCTGTCCGGGCTTGAGACTCAATGCTGTAGCATATTACCGGGCCCT	2988
Db	2941	GAGCTCGCCGGGAGAGCTGTCCGGGCTTGAGACTCAATGCTGTAGCATATTACCGGGCCCT	3000
QY	2989	GATGATATCCGTCATACCAACTATGACGGAGAGCTATGTGTGACACAGGACGCTATATG	3048
Db	3001	GATGATATCCGTCATACCAACTATGACGGAGAGCTATGTGTGACACAGGACGCTATATG	3060
QY	3049	ACGGGCTTTTACCGGCGGATTTGCACTAGTATGATCGACTCAATATATGTGTCAACCCAGCA	3108
Db	3061	ACGGGCTTTTACCGGCGGATTTGCACTAGTATGATCGACTCAATATATGTGTCAACCCAGCA	3120
QY	3109	GTCGACTTACGCGCTTGAGCCCGGACCTTCACCATATGACACAGCAGCGTCCACAGACAGCG	3168
Db	3121	GTCGACTTACGCGCTTGAGCCCGGACCTTCACCATATGACACAGCAGCGTCCACAGACAGCG	3180
QY	3169	GTGTACGCTTGCGACGGGCGGACGAGGACGAGTGGGAGGATGGGATTTTACAGGTTT	3240
Db	3181	GTGTACGCTTGCGACGGGCGGACGAGGACGAGTGGGAGGATGGGATTTTACAGGTTT	3240
QY	3229	GTGACTCCAGAGACAGCGCCCTCGGGCATGTTTGATTCCTCGTTCTGTGGAGAGTCAAT	3288
Db	3241	GTGACTCCAGAGACAGCGCCCTCGGGCATGTTTGATTCCTCGTTCTGTGGAGAGTCAAT	3300
QY	3289	GACGGGGCTGTGCTGTGGTACAGAGCTACAGCCCGCCGABACCTCACTAGTTAGTGGGGCT	3348
Db	3301	GACGGGGCTGTGCTGTGGTACAGAGCTACAGCCCGCCGABACCTCACTAGTTAGTGGGGCT	3360
QY	3349	TACCTAAACACACAGGAGTTGCCCGCTGTGCAGAGACATCTGGAATTTGTGGAGAGCCTC	3408
Db	3361	TACCTAAACACACAGGAGTTGCCCGCTGTGCAGAGACATCTGGAATTTGTGGAGAGCCTC	3420
QY	3409	TTTACAGGCGTACCCCACTAGAGCGCCATTTCTGTCCBACATCAAGCAGGACGAGAAAC	3468
Db	3421	TTTACAGGCGTACCCCACTAGAGCGCCATTTCTGTCCBACATCAAGCAGGACGAGAAAC	3480
QY	3469	AACTTCCCTACCTGTAGATATACAGAGCTACGGTGTGCGCAGGAGCTACGGCTTCACCT	3528
Db	3481	AACTTCCCTACCTGTAGATATACAGAGCTACGGTGTGCGCAGGAGCTACGGCTTCACCT	3540
QY	3529	CCATGTGTGGACCAAAATGTGGAAGTGTCTATACGGCTTAACGCTACGCTGACGGGCA	3588
Db	3541	CCATGTGTGGACCAAAATGTGGAAGTGTCTATACGGCTTAACGCTACGCTGACGGGCA	3600
QY	3589	ACGCCCTGTGTATAGGTGGAGGCCGTTCAAAACAGAGTTACTACACACACCCCATTA	3648
Db	3601	ACGCCCTGTGTATAGGTGGAGGCCGTTCAAAACAGAGTTACTACACACACCCCATTA	3660

QY	3649	ACAAATATCATGACGATGATCATGTGGCGTACGCTGGAGAGTGTATACAGACACTGGGTG	3708
Db	3661	ACCAATATCATATGAGCATCATGATGTGGCGTACGCTGGAGAGTGTATACAGACACTGGGTG	3720
QY	3709	CTGTATGGCGGAGTCCCTATAGCAGCTCTGGCCGCTATTTGGCTGACAAACAGCGTGGTC	3768
Db	3721	CTGTATGGCGGAGTCCCTATAGCAGCTCTGGCCGCTATTTGGCTGACAAACAGCGTGGTC	3780
QY	3769	ATTGTGGGCGAGATCATCTGTGTCCGGAGGCGCGGCATATTTCCCGACAGGGAATCCTT	3828
Db	3781	ATTGTGGGCGAGATCATCTGTGTCCGGAGGCGCGGCATATTTCCCGACAGGGAATCCTT	3840
QY	3829	TACCGGGAGTTTCATGTAGATGGAAGAGATGGCGCTCCACACCTCCCTTACATGGAAACGGA	3888
Db	3841	TACCGGGAGTTTCATGTAGATGGAAGAGATGGCGCTCCACACCTCCCTTACATGGAAACGGA	3900
QY	3889	ATGCAAGTCCGCGCGAACAATTCAAAACAGAAAGCAATCGGTTGTCTGTCAAAAGCCACAG	3948
Db	3901	ATGCAAGTCCGCGCGAACAATTCAAAACAGAAAGCAATCGGTTGTCTGTCAAAAGCCACAG	3960
QY	3949	CAAGCGAGAGCTGTGCTGCCGCTGGTGGAAATCCAAATGGCGGAAACCTCGAAGCCTTCTGG	4008
Db	3961	CAAGCGAGAGCTGTGCTGCCGCTGGTGGAAATCCAAATGGCGGAAACCTCGTCTTGG	4020
QY	4009	GGAGGCAATATGTGGAAATTTATCAGCGGGATTCATATTTAGCAGGCTGTGCCCTGTG	4068
Db	4021	GGAGGCAATATGTGGAAATTTATCAGCGGGATTCATATTTAGCAGGCTGTGCCCTGTG	4080
QY	4069	CCTGGCAACCCCGGATAGATCATCATGTATGCATTCAACGCTTATCAACGACCCGCTC	4128
Db	4081	CCTGGCAACCCCGGATAGATCATCATGTATGCATTCAACGCTTATCAACGACCCGCTC	4140
QY	4129	ACCACCCAAATPACCCTTCGTTTAAATCTCTGGGGGAAATGGATGGCCGCCCAACTTCT	4188
Db	4141	ACCACCCAAATPACCCTTCGTTTAAATCTCTGGGGGAAATGGATGGCCGCCCAACTTCT	4200
QY	4189	CCTCCACAGCGTGTCTGTCTTGTATAGCGCGCGCATCGCTGAGACGAGCTTTGGACGC	4248
Db	4201	CCTCCACAGCGTGTCTGTCTTGTATAGCGCGCGCATCGCTGAGACGAGCTTTGGACGC	4260
QY	4249	ATAGGCGCTTGGGAAGGAGCTGTGGATATTTTGGCAGGTTATAGAGACAGGAGTGGCAGGC	4308
Db	4261	ATAGGCGCTTGGGAAGGAGCTGTGGATATTTTGGCAGGTTATAGAGACAGGAGTGGCAGGC	4320
QY	4309	GCGCTGTGSCCTTTAAGTCTATAGCGCGGAGATGCCCTCCACGAGGACTGTGCTAAC	4368
Db	4321	GCGCTGTGTGSCCTTTAAGTCTATAGCGCGGAGATGCCCTCCACGAGGACTGTGCTAAC	4380
QY	4369	CTACCTCCTGCTATTCCTCTCCCGCGGGCGCCATGTAGTGGGGGTGTGTGGCAGCAGTA	4428
Db	4381	CTACCTCCTGCTATTCCTCTCCCGCGGGCGCCATGTAGTGGGGGTGTGTGGCAGCAGTA	4440
QY	4429	CTGCGTGGCACGTGGGCCACAGGGGAGGGGCTGTGCTACATGATGAACCGGCTGATACG	4488
Db	4441	CTGCGTGGCACGTGGGCCACAGGGGAGGGGCTGTGCTACATGATGAACCGGCTGATACG	4500
QY	4489	TTTCGCTTGGCGGGTAAACAGAGTGTCCCCAGCAGCATATGTGCTGTAGAGCAGCAGCTCA	4548
Db	4501	TTTCGCTTGGCGGGTAAACAGAGTGTCCCCAGCAGCATATGTGCTGTAGAGCAGCAGCTCA	4560
QY	4549	GCACGTGTCACTCAATCTCTCTAGTCTTACCATCACTCAGCTGTCTGAAGAGCTTAC	4608
Db	4561	GCACGTGTCACTCAATCTCTCTAGTCTTACCATCACTCAGCTGTCTGAAGAGAGCTTAC	4620
QY	4609	CAGTGGATCAACGAGAGCTGCTCACGCCATGCTCGGCTGCGGCTGTAGAGATTTTGG	4668
Db	4621	CAGTGGATCAACGAGAGCTGCTCACGCCATGCTCGGCTGCGGCTGTAGAGATTTTGG	4680
QY	4669	GATTGTGATATGACAGGCTGTGACATGATTTAABAAGCTGGCTCAGTCCAGAGCTCTGCGC	4728
Db	4681	GATTGTGATATGACAGGCTGTGACATGATTTAABAAGCTGGCTCAGTCCAGAGCTCTGCGC	4740
QY	4729	CAATTGCGGGAGTCCCTTCTTCTCATATGTCAACGTGGGTTACAAAGGAACTTGGCGGGGC	4788

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Db 4741 CGATTGCCGGAGAGTCCCTTTCTTCATGTCACAGTGGTATCAAGAGAGTCTGGCGGGC 4800
QY 4789 GACGGCATCATGCAAAACCCTGCCCATGTGGAGACAGATCACCGGACATGTGAAAAA 4848
Db 4801 GACGGCATCATGCAAAACCCTGCCCATGTGGAGACAGATCACCGGACATGTGAAAAA 4860
QY 4849 GGTTCATGAGATGCTGGGGCTAGGACCTGTAGTAAAGCTGGGATGGAATTCGCC 4908
Db 4861 GGTTCATGAGATGCTGGGGCTAGGACCTGTAGTAAAGCTGGGATGGAATTCGCC 4920
QY 4909 ATTAACGGGTACACACCGGGCCCTGCAAGCCCTCCCGGGCCCAATTATTCAGGGC 4968
Db 4921 ATTAACGGGTACACACCGGGCCCTGCAAGCCCTCCCGGGCCCAATTATTCAGGGC 4980
QY 4969 CTGTGGCGGGTGGCTGCTGAGAGATGAGTGGATGAGGGGGGATTCCTCACTAG 5028
Db 4981 CTGTGGCGGGTGGCTGCTGAGAGATGAGTGGATGAGGGGGGATTCCTCACTAG 5040
QY 5029 GTGACGGGCATGACCACTGACAAAGTAAAGTGCCTGTAGGTTCCGGCCCCGGAATTC 5088
Db 5041 GTGACGGGCATGACCACTGACAAAGTAAAGTGCCTGTAGGTTCCGGCCCCGGAATTC 5100
QY 5089 TTCACAGAAGTGTAGGGGGTGGCGTTGACAGGTACGCTCCAGGTGCAAAACCCCTCCTA 5148
Db 5101 TTCACAGAAGTGTAGGGGGTGGCGTTGACAGGTACGCTCCAGGTGCAAAACCCCTCCTA 5160
QY 5149 CGGGAGAGGTTCACATTCCTGTGGGGCTCAATCAATACCTGTTGGGTACAGCTCCCA 5208
Db 5161 CGGGAGAGGTTCACATTCCTGTGGGGCTCAATCAATACCTGTTGGGTACAGCTCCCA 5220
QY 5209 TGGGAGCCCGAACCAGAGTACAGTGTCACTTCATGCTCAACGACCCCTCCCAATTC 5268
Db 5221 TGGGAGCCCGAACCAGAGTACAGTGTCACTTCATGCTCAACGACCCCTCCCAATTC 5280
QY 5269 AGGGGGAGAGGGCTTAAGCGTAAAGTGGSCAGGGGATCCGCCCTCTTGGCCAGTCA 5328
Db 5281 AGGGGGAGAGGGCTTAAGCGTAAAGTGGSCAGGGGATCCGCCCTCTTGGCCAGTCA 5340
QY 5329 TCAGTACGCCAGCTGTCTGGCCCTTCTTGAAGGCAACATCACTACCCGTCACTATTC 5388
Db 5341 TCAGTACGCCAGCTGTCTGGCCCTTCTTGAAGGCAACATCACTACCCGTCACTATTC 5400
QY 5389 CCGGAGCGTACCTCATGAGAGCCAACTCTGTGGCGGAGAGATGGGCGGGAATTC 5448
Db 5401 CCGGAGCGTACCTCATGAGAGCCAACTCTGTGGCGGAGAGATGGGCGGGAATTC 5460
QY 5449 ACCCGGTGAGTCAAAAAATTAAGTAAATTTTGGACTCTTTCGAGCGGCTCCAAAGC 5508
Db 5461 ACCCGGTGAGTCAAAAAATTAAGTAAATTTTGGACTCTTTCGAGCGGCTCCAAAGC 5520
QY 5509 GAGGAGATGAGAGGAGATACCGTTCGGGGGAGATCCGAGAGTCCGAGAAATTC 5568
Db 5521 GAGGAGATGAGAGGAGATACCGTTCGGGGGAGATCCGAGAGTCCGAGAAATTC 5580
QY 5569 CCTGAGCGATCCCATATGAGGACGCGCGGATTAACAACCTCCACTGTTAGATCTCG 5628
Db 5581 CCTGAGCGATCCCATATGAGGACGCGCGGATTAACAACCTCCACTGTTAGATCTCG 5640
QY 5629 AAGGAGCCCGAGTACGTCCCTCCATGATGATACAGGGGTCCATTTGCCCGCAAGCC 5688
Db 5641 AAGGAGCCCGAGTACGTCCCTCCATGATGATGATACAGGGGTCCATTTGCCCGCAAGCC 5700
QY 5689 CCTCCGATACCACTCCAGAGAGAGAGAGGTTGTCTGTAGATCAATCCGTCTCT 5748
Db 5701 CCTCCGATACCACTCCAGAGAGAGAGAGGTTGTCTGTAGATCAATCCGTCTCT 5760
QY 5749 TCTGCTTGGCGAGCTGCGCCACAAGACCTTCGAGACTCCGAATCTGCGCGTGCAC 5808
Db 5761 TCTGCTTGGCGAGCTGCGCCACAAGACCTTCGAGACTCCGAATCTGCGCGTGCAC 5820
QY 5809 AGCGGACGCAAGGCTCTCTGACAGCCCTCGAGAGAGGCGAGAGCGGAGATCCGAC 5868
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Db 5821 AGCGGACGCAAGGCTCTCTGACAGCCCTCCGAGACGAGCGGACGCGGATCCGAC 5880
QY 5869 GTTAGTGTACTCTCTCCATGCCCCCTTGAAGGGGAGCGCGGGGATCCGATCTCAAC 5928
Db 5881 GTTAGTGTACTCTCTCCATGCCCCCTTGAAGGGGAGCGCGGGGATCCGATCTCAAC 5940
QY 5929 GACGGTCTTGGTCTACCGTAAAGCGAGAGCTAGTAGAGACGTCTGCTGCTGATG 5988
Db 5941 GACGGTCTTGGTCTACCGTAAAGCGAGAGCTAGTAGAGACGTCTGCTGCTGATG 6000
QY 5989 TCTTACACATGAGAGGCGCCCTGATACGCCATGCGCTCGGAGAGAAACCAAGCTGCC 6048
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QY 6049 ATCAATGACATGAGCACTCTTGTCTCGTACACACCACTTGTATGCTACACATCT 6108
Db 6061 ATCAATGACATGAGCACTCTTGTCTCGTACACACCACTTGTATGCTACACATCT 6120
QY 6109 CGCAGCGCAACCTGCGGAGAGAGAGTCACTTTGACAGACTGCAAGTCTCTGGACGAC 6168
Db 6121 CGCAGCGCAACCTGCGGAGAGAGAGTCACTTTGACAGACTGCAAGTCTCTGGACGAC 6180
QY 6169 CACTACCGGAGCGTCTCAAGAGATGAGAGAGCGAGGCTCCACAGTTAAGCTAAACTT 6228
Db 6181 CACTACCGGAGCGTCTCAAGAGATGAGAGAGCGAGGCTCCACAGTTAAGCTAAACTT 6240
QY 6229 CTATCTGTGAGAAACCTGTAACTGACGCCCCACATTTGGCCAGATCTAAATTTGGC 6288
Db 6241 CTATCTGTGAGAAACCTGTAACTGACGCCCCACATTTGGCCAGATCTAAATTTGGC 6300
QY 6289 TATGGGGCAAGAGAGTGGCGGACCTTACAGCAAGGCGCTTAACACATCCGCTCGTG 6348
Db 6301 TATGGGGCAAGAGAGTGGCGGACCTTACAGCAAGGCGCTTAACACATCCGCTCGTG 6360
QY 6349 TGGAGGACTTGTGAGAGACTAGACACCAATTAACAACCAATCATGCAAAAAAT 6408
Db 6361 TGGAGGACTTGTGAGAGACTAGACACCAATTAACAACCAATCATGCAAAAAAT 6420
QY 6409 GAGGTTTCTGGTCCACACAGAGAGGGGGCGGCAAGCAGTGCCTTATGATTC 6468
Db 6421 GAGGTTTCTGGTCCACACAGAGAGGGGGCGGCAAGCAGTGCCTTATGATTC 6480
QY 6469 CCAGATTTGGGGTTCGTGTGTGCGAGAAATGGCCCTTAAGATGTGTCTCCACCCTC 6528
Db 6481 CCAGATTTGGGGTTCGTGTGTGCGAGAAATGGCCCTTAAGATGTGTCTCCACCCTC 6540
QY 6529 CCTCAGGCGGTATGGGCTTTCATACGAGATTCATTAATCTCTGAGACGCGGTGAG 6588
Db 6541 CCTCAGGCGGTATGGGCTTTCATACGAGATTCATTAATCTCTGAGACGCGGTGAG 6600
QY 6589 TTCCTGTGAATGCTTGAAAGCGAGAAATGGCCCTTATGAGCTTCAATGACCCCG 6648
Db 6601 TTCCTGTGAATGCTTGAAAGCGAGAAATGGCCCTTATGAGCTTCAATGACCCCG 6660
QY 6649 TGTTTTGACTACAGGCTACGATGATACATCCGTGTGAGAGTCAATCTACCAATGT 6708
Db 6661 TGTTTTGACTACAGGCTACGATGATACATCCGTGTGAGAGTCAATCTACCAATGT 6720
QY 6709 TGTGATTTGGCCCCGAGAGCCAGACAGGCTTAAGTGGCTCAAGAGCGGCTTACATC 6768
Db 6721 TGTGATTTGGCCCCGAGAGCCAGACAGGCTTAAGTGGCTCAAGAGCGGCTTACATC 6780
QY 6769 GGGGGGCCCCGAGTAAATTTTAAGGCAAGATGGGCTATGCGCGGTGCGCGGAGC 6828
Db 6781 GGGGGGCCCCGAGTAAATTTTAAGGCAAGATGGGCTATGCGCGGTGCGCGGAGC 6840
QY 6829 GGTGTACTGAGACCGAGCGGGTAAATACCTCAATGTTACTTGAAGCGGCTGCGGCC 6888
Db 6841 GGTGTACTGAGACCGAGCGGGTAAATACCTCAATGTTACTTGAAGCGGCTGCGGCC 6900
QY 6889 TGTGAGCTGCAAGCTCCAGAGTCAAGATGCTGTATGCGAGAGACGACTTGTGTT 6948
Db 6901 TGTGAGCTGCAAGCTCCAGAGTCAAGATGCTGTATGCGAGAGACGACTTGTGTT 6960
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QY	6949	ATTGTTAAAGCCGGGGAGCCCAAGAGAGAGGGGAGCTTACACGGGCTTCACGGAGGCT	7000
Db	6961	ATTGTTAAAGCCGGGGAGCCCAAGAGAGAGGGGAGCTTACCGGCTTCACGGAGGCT	7020
QY	7009	ATGACTGATACTCTGCCCCCTCCCTGGGGAGCCCGCCCAACGAAATACGACTTGGATTG	7068
Db	7021	ATGACTGATACTCTGCCCCCTCCCTGGGGAGCCCGCCCAACGAAATACGACTTGGATTG	7080
QY	7069	ATTACATCATGCTCTCTCCCATGTGTGTAGTGGGCAAGATGCACTGGCAAAAGGCTTAC	7128
Db	7081	ATTACATCATGCTCTCTCCCATGTGTGTAGTGGGCAAGATGCACTGGCAAAAGGCTTAC	7140
QY	7129	TATCTCACCCGTGACCCACACCCACCCCTCTTGCGGGGGCTGCGTGGGAGACGCTAGACAC	7188
Db	7141	TATCTCACCCGTGACCCACACCCACCCCTCTTGCGGGGGCTGCGTGGGAGACGCTAGACAC	7200
QY	7189	ACTCCATCATTCCTCTGGCTAGGCAACATCATATGTAAGCCCCACTTGTGGGCAAG	7248
Db	7201	ACTCCATCATTCCTCTGGCTAGGCAACATCATATGTAAGCCCCACTTGTGGGCAAG	7260
QY	7249	ATGATCTCGATGACTCATTTCTCTCCATCTTTCTAGCTCAGGAACAACCTGAAAAGCC	7308
Db	7261	ATGATCTCGATGACTCATTTCTCTCCATCTTTCTAGCTCAGGAACAACCTGAAAAGCC	7320
QY	7309	CTACATTTGTAGATCTACGGGGGCTTPTACTCATTTAGACCCACTTGACCTACCTCAGATC	7368
Db	7321	CTACATTTGTAGATCTACGGGGGCTTPTACTCATTTAGACCCACTTGACCTACCTCAGATC	7380
QY	7369	ATTACAGACTCCATGAGCTTTAGCGCATTTTCACTCCATAGTACTCTCCAGGTGAGATC	7428
Db	7381	ATTACAGACTCCATGAGCTTTAGCGCATTTTCACTCCATAGTACTCTCCAGGTGAGATC	7440
QY	7429	AATAGGGGGTTTATCCCTCAGAGAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACAT	7488
Db	7441	AATAGGGGGTTTATCCCTCAGAGAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACAT	7500
QY	7489	CGGGCCAGAAAGTGTCCGGCTAGGCTACTGTGCCAAGGGGGAGGGCTGCCACTTGTGGC	7548
Db	7501	CGGGCCAGAAAGTGTCCGGCTAGGCTACTGTGCCAAGGGGGAGGGCTGCCACTTGTGGC	7560
QY	7549	AAGTACCTCTTCACTGGGAGTAAGGACCAAGCTCAACTCACTCAATCCCGGCTGGC	7608
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QY	7849	TTTTTCTCTTTTTTTTTCCTTTTTTTTTTCTTTTCTTTTCTTCTTGGTGGCTTCACCTTAC	7908
Db	7861	TTTTTCTCTTTTTTTTTCCTTTTTTTTTTCTTTTCTTTTCTTCTTGGTGGCTTCACCTTAC	7920
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Db	7921	CCTACTCAAGGCTAGCTGTGAAGAGTCCGTGAGCCCTTGACTGTGAGAGAGTGTGATAC	7980
QY	7969	TGGCTCTCTGCAAGTCAAGT 7989	
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DEFINITION	Sequence 2 from Patent EP1043399.				
ACCESSION	AX036253				
VERSION	AX036253.1	GI:11225869			
KEYWORDS					
SOURCE	Hepatitis C virus.				
ORGANISM	Hepatitis C virus.				
REFERENCE	1 (bases 1 to 8637)				
AUTHORS	Bartenschlager, R.D.				
TITLE	Hepatitis C virus cell culture system				
JOURNAL	Patent: EP 1043399-A 2 11-OCT-2000;				
FEATURES	BARTENSCHLAGER RALF DR (DE)				
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ORIGIN					
Query Match	91.6% Score 7324.6; DB 6; Length 8637;				
Best Local Similarity	92.5% Pred No. 0;				
Matches 7985; Conservative	0; Mismatches 4; Indels 648; Gaps 1;				
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Db	1 GCCAGCCCCCGATTGGGGGGGACACTCCACCATATAGTACTCCCTGTGAGAACTACTG 60				
QY	61 TCTTCAGCGAANAAGCGTCTAGCCANTGGGTAGATAGTGTGTGCACCCCAAGGAC 120				
Db	61 TCTTCAGCGAANAAGCGTCTAGCCANTGGGTAGATAGTGTGTGCACCCCAAGGAC 120				
QY	121 CCCCCCTCCCGGGAGAGCCATAGTGTGTGCGGGAACCGGTAGTAGTACCCGGAATTGCCAG 180				
Db	121 CCCCCCTCCCGGGAGAGCCATAGTGTGTGCGGGAACCGGTAGTAGTACCCGGAATTGCCAG 180				
QY	181 GAGCAGCCGGGTCTTTTCTTGATCAACCCCGTCAATGCGCTGGAGATTGGCGTGGCCCC 240				
Db	181 GAGCAGCCGGGTCTTTTCTTGATCAACCCCGTCAATGCGCTGGAGATTGGCGTGGCCCC 240				
QY	241 GCGAGACTGCTAGCCGCGAGTAGTGTGTGGGTGCGGAAGGCCCTTGTGTACTGCTGATAGG 300				
Db	241 GCGAGACTGCTAGCCGCGAGTAGTGTGTGGGTGCGGAAGGCCCTTGTGTACTGCTGATAGG 300				
QY	301 GTGCTTGGCAGATGCCCGGGAGAGTCTCGTAGACGCTGACCATATAGCAGCAATCCTAAAC 360				
Db	301 GTGCTTGGCAGATGCCCGGGAGAGTCTCGTAGACGCTGACCATATAGCAGCAATCCTAAAC 360				
QY	361 CTCAAAAGAAAACCAAGAGGCGCGGCATATTGAACAAGATGGAATTGCACGCAAGTTCTC 420				
Db	361 CTCAAAAGAAAACCAAGAGGCGCGGCATATTGAACAAGATGGAATTGCACGCAAGTTCTC 420				
QY	421 CGGCCGCTTGGGTGAGAGAGCTATTGGCTATAGACTTGGGACACACAGACATCGGCTGCT 480				
Db	421 CGGCCGCTTGGGTGAGAGAGCTATTGGCTATAGACTTGGGACACACAGACATCGGCTGCT 480				
QY	481 CTGATGCGCGGCTTCCGCGTGTCAAGCCACAGGGGCGCCGCTTCTTTTGTACAGACG 540				
Db	481 CTGATGCGCGGCTTCCGCGTGTCAAGCCACAGGGGCGCCGCTTCTTTTGTACAGACG 540				
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Db	1981	CGCGATGCGCTACCTCTCTCACGTGCGGATGCACCCAGAGCTAATCTTACCATACC	2040
QY	1804	-----	1803
Db	2041	AAAACTTGTCTGCCATATCTGGTCCACTCACTATGTTGCTCCAGGCTGTATATCAAAATG	2100
QY	1804	-----	1803
Db	2101	CCGTACTTCGTGGCGGACACAGGGGCTCATTGTCGATGCATGCTGTGGCGAAGTTGCT	2160
QY	1804	-----	1803
Db	2161	GGGGTCAATTATGTCCAAATGGCTCTTCATGAAAGTTGGCCGCACTACAGTACTAGTT	2220
QY	1804	-----	1803
Db	2221	TATGACCATCTCACCCCATCTGCGGAGCTAGGCCACAGCGGGGCTACGAGACTTGGGTG	2280
QY	1804	-----	1803
Db	2281	GCAGTTGAGCCCGTCTGTCTTCTGTATATGGAGACCAGAGTTATCACTGGGAGGAGAC	2340
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QY	1933	CTGGGACCTGCGTCAATGGCGTGTGTGGACTGTCTATCATGTGTCGGGCTCAAGACCC	1992
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Db	2821	GGGAGCTTACTCTCCCCAGGCCCGTCTCTACTTAAAGGCTCTTGGGGGTGTCACTG	2880

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QY	2233	CTTGCCCTCTGGGGGACAGCTGTGGGCACTCTTCGGGGCTCCGTGTGCACCCGAGGGGT	2232
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Db	2941	GGCAAGGCGGTGGACCTTTGTAACCGTGTGAGTGTATGGAACCACTATCGGGTCCCCGGTC	3000
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QY	2413	GGCCCTACTGGTAGCGGCAGAGCACTAAGGTTCGGGCTGCCTATATGACGCCAAGGTAT	2472
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QY	2593	CCCATCACGTAATCCACCTTATGGCAAGTTCTTGCCGACGGTGTGCTGTGGGGGCC	2652
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Db	4081	GCCCATTTCTTGTCACGACTAAGCAGGAGACAGCAACTTCCCTACTCTGGTGCATAC	4140
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QY 4753 TCATGTCAACGTGGGTACAAGGAGTCTGGCGGGGAGCGGCATCTGCAAAACCACTGC 4812
Db 5401 TCATGTCAACGTGGGTACAAGGAGTCTGGCGGGGAGCGGCATCTGCAAAACCACTGC 5460
QY 4813 CCATGTGAGACAGATACCGGACATGTGAAAAAGGTTCCATGAGATGCTGGGGCT 4872
Db 5461 CCATGTGAGACAGATACCGGACATGTGAAAAAGGTTCCATGAGATGCTGGGGCT 5520
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Db 5521 AGGACCTGTGTAAACAGCTGGACATGACATTCCTCCATTAAACCGTACACACGGGGCTCC 5580
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 Lohmann, V., Koller, F., Koch, J., Herian, U., Theilmann, L. and
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 Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell
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 Bartenschlager, R.
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QY	3073	TCAGTATGATGATGATATACATGATGTCACCCAGAGTGCATTCAGCTGTGACCCGAC	3132
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Db	4201	TGTCATACAGGCTTAAAGCTTACGCTGACGCGGCAAGCGCCCTGCTATAGGCTGGGA	4260
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Db	4381	CTGGCGCGTATGCTGCTACACAGGAGCGAGCTGCTCATTTGGGACAGATCATCTGTCC	4440
QY	3793	GGAAGCGCGGATCATCTTCCGACAGAGGAACTCTTTACCGGAGTTCATGAGATGAA	3852
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QY	4273	GATATTTTGGCAGTTATGAGACAGGAGGTCAGGCGCTGCTGAGGCTTTAAGTATG	4332
Db	4921	GATATTTTGGCAGTTATGAGACAGGAGGTCAGGCGCTGCTGAGGCTTTAAGTATG	4980
QY	4333	AGGCGGAGATGCTTCCACAGAGACCTGCTTAACCTACTCCCTGCTATCTCTCCCT	4392
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 TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
 JOURNAL Science 285 (5424), 110-113 (1999)
 MEDLINE 99322193
 PUBMED 10390360
 REFERENCE 2 (bases 1 to 8649)
 AUTHORS Bartenschlager,R.
 TITLE Direct Submission
 JOURNAL Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY
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 ORGANISM Hepatitis C virus.
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 REFERENCE 1
 AUTHORS Kuxolj, G. and Pause, A.
 TITLE Self-replicating rna molecule from hepatitis C virus
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ACCESSION AX472314
VERSION AX472314.1 GI:22207333
KEYWORDS
SOURCE Hepatitis C virus.
ORGANISM Hepatitis C virus.
REFERENCE 1
AUTHORS Kuo, J. G. and Pause, A.
TITLE Self-replicating RNA molecule from hepatitis C virus
JOURNAL Patent: WO 02052015-A 24 04-JUL-2002;
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VGVGIVLIPNR"
BASE COUNT 1770 a 2556 c 2439 g 1873 t
ORIGIN
Query Match 90.9%; Score 7266.4; DB 6; Length 8638;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 7971; Conservative 0; Mismatches 6; Indels 671; Gaps 3;
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QY 362 TCAAGAAAAACCAAGGCGCGCATATTTAGACAGATGATTTGACGAGTCTCC 421
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DB 602 GACGGGGCTTCCTTGGCAGCTGTGCTCGACGTTGTCTACTGAAGCGGGAAGGAGCTGCT 661
QY 662 GCTATTGGGGAGAGTGGCGGGGAGAGATCTCTGTCATCTCACTGACCTTGTCTGCGGAGAA 721
DB 662 GCTATTGGGGAGAGTGGCGGGGAGAGATCTCTGTCATCTCACTGACCTTGTCTGCGGAGAA 721
QY 722 AGTATCCATCATGAGCTGATGCAATGGCGGCGCTGATACGCTTGATCGGCTACCTGCC 781
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DB 782 ATTGACACCAACGGAACATGSCATGAGGAGGACGATGAGTGAAGCGGCT 841
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QY 1611 AAGAGTCAATGCTCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGATGCCAAGG 1670
DB 1611 AAGAGTCAATGCTCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGATGCCAAGG 1670
QY 1670 TACCCCATTTGATGGATGATGATCTGGGGCTGCGGAGTGCATGCTTACATGTGTTAGT 1729
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QY 2571 CACATATCTTCTGCGGAGCTGCTGCAATGAGGCTTGTGAGTGTATCATGATGAGCG 2630
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DB 2631 GCTCAAGACCTTGGCGGCGCAAGGAGGCGCAATCACCAATGTATACCAATGTGAGCC 2690
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DB 2042 AAGACCTGTGCGGCTGCGAAGCGGCGGCGGCTTCTTGTACACCATGACCTGCG 2101

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QY 2102 GCAGCTCGGACCTTTACTTGGTACAGAGGATGCGCATGTGCTCATTCGCGGCGCGGGG 2161
Db 2751 GCAGCTCGGACCTTTACTTGGTACAGAGGATGCGCATGTGCTCATTCGCGGCGCGGG 2810
QY 2162 GCAGCAGCAGGGGAGGCTACTCTCCCGAGGCGCGCTCTCTACTTGAAGGGCTCTTGG 2221
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QY 2222 GCGGTCACCTGCTCTGCGGCTCGGGGAGGCTGTGGGCACTTTCGGGCTGCGGCTGCA 2281
Db 2871 GCGGTCACCTGCTCTGCGGCTCGGGGAGGCTGTGGGCACTTTCGGGCTGCGGCTGCA 2930
QY 2282 CCCGAGGGGTTGCGAAGGCGGTGAGCTTTGTACCCGTCGAGTCTATGGAACCACTATGC 2341
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QY 2402 CCCATCTACAGGCGCCCTACTGAGTAGCGGCAAGAGCACTAAGGTGCGGCTGCTATGCA 2461
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Db 3531 AAGGGGGGAGGACCTCATTTTCTGCACTTCCAGAAAGAAATGTGATGACTGCGCGCA 3590
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QY 3002 TACCAACTAGGAGAGAGCTATGTGCTAGCAAGGAGGCTCTATATAGCGGCTTACG 3061
Db 3651 TACCAACTAGGAGAGAGCTATGTGCTAGCAAGGAGGCTCTATATAGCGGCTTACG 3710
QY 3062 GCGATTGAGTCAAGTATGAGTCACTGATCATATGCTATGCTATGCTATGCTATGCTATG 3121
Db 3711 GCGATTGAGTCAAGTATGAGTCACTGATCATATGCTATGCTATGCTATGCTATGCTATG 3770
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QY 3602 ATAGGCTGAGGAGCGGTTCAAAACAGAGTACTACACACACCCCATACCAATATACATCA 3661
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QY 3722 TCCTAGCAGCTGTGGCGCGATTTGCTGTACAAACAGGACGCTGTGATTTGTGGGAGGA 3781
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QY 3782 TCATTTGTTCGGGAGAGCGCGGCTCATCTCCGAGAGGAGTCTTACCGGAGGTGCG 3841
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QY 3902 AACAATTTAAACAGAGGCAATGGGGTTGTCTGCAAAAGGCAACCAAGGAGGAGGCTG 3961
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Db 4851 CTTCTGCTTGTGTAGGCGCGGCACTGCTGAGGCGGCTGTGTGGAGCATAGGCGCTTGGGA 4910
|||||

QY	4262	AGGCGCTGTGCATATTTTGGAGGTTATAGAGACAGGGGGTGGCAGGGCGGCTGTGGGCT	4322
Db	4911	AGATGGCTTGGGATATTTTGGCAGGTTATGGAGCAGGGGGTGGCAGGGCGGCTGTGGGCT	4970
QY	4322	TTAAGGTCATGAGCGCGAGATAGCCCTCCACCGAGGACCTGGCTAACTACTCCCTGTA	4381
Db	4371	TTAAGGTCATGAGCGCGAGATAGCCCTCCACCGAGGACCTGGCTAACTACTCCCTGTA	5030
QY	4382	TCCTTCCTCCCTGGCGCCCTAGTCGTGCGGGGGTGGTGGCGAGGATACTCGTCGACAG	4441
Db	5031	TCCTTCCTCCCTGGCGCCCTAGTCGTGCGGGGGTGGTGGCGAGGATACTCGTCGCGACG	5090
QY	4442	TGGGCCAGGGGAGGGGCGCTGTGCAGTGAACCGGCTGTATAGCGTTGCTTCGCGGG	4501
Db	5091	TGGGCCAGGGGAGGGGCGCTGTGCAGTGAACCGGCTGTATAGCGTTGCTTCGCGGG	5150
QY	4502	GTAACCCAGGTCCTCCCGCAGCACTATAGTCGCGAGAGAGGACGCGTGCACGTCACTC	4561
Db	5151	GTAACCCAGGTCCTCCCGCAGCACTATAGTCCTGAGAGGAGAGCGCTGCAGCACTGTCACTC	5210
QY	4562	AGATCTCTCTAGTCTTACCACTACTCACTCTCTGAGAGAGCTTCACCACTGATGATCAAG	4621
Db	5211	AGATCTCTCTAGTCTTACCACTACTCACTCTCTGAGAGAGCTTCACCACTGATGATCAAG	5270
QY	4622	AGGACTCTCTCAGCGCATGGTCGCGCTGTGCTGCTAAGAGATGTTGGGATTTGGATATGCA	4681
Db	5271	AGGACTCTCTCAGCGCATGGTCGCGCTGTGCTGCTAAGAGATGTTGGGATTTGGATATGCA	5330
QY	4682	CGGTTGTAGCTGATTTCAAGACCTGGCTCCAGTCCCACTCTCTGCGCGATTTGCCGGGAG	4741
Db	5331	CGGTTGTAGCTGATTTCAAGACCTGGCTCCAGTCCCACTCTCTGCGCGATTTGCCGGGAG	5390
QY	4742	TCCCTTCCTCTCATGTGCACAGTGGGTACAAAGGAGTGTGGCGGGGCGACGGCATCTATGC	4801
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SOURCE					
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REFERENCE		1			
AUTHORS	Kukolj,G. and Pause,A.				
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JOURNAL	Patent: WO 02052015-A 7 04-Jul-2002;				
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Query Match 90.7% Score 7246.6: DB 6: Length 8638:
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Search completed: May 31, 2003, 12:05:03
 Job time : 13261 secs

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Page 1

Hepatitis C virus	100
Hepatitis C virus	100
Hepatitis C virus	100
Hepatitis C virus	100

Hepatitis C virus

Hepatitis C virus
Hepatitis C virus
Hepatitis C virus
Hepatitis C virus

Hepatitis C virus
Hepatitis C virus
HCV-S1 full-length
Infectious hepatitis

Infectious Hepatitis
Blood Transmissible

Non-A, non-B viral
Non-A, non-B viral
Full-length Hepati
Non-A non-B hepat

Korean hepatitis C
Hepatitis C virus
HCV associated with

Partial HCV non-structural protein 3
Hepatitis C virus
DNA encoding HCV protein 3
Human hepatitis C virus

NANBHV E1/E2 gene

[illegible]

FT	/tag=	b
FT	/product=	"NS3 protease/helicase"
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PN	WO200238793-A2.	
XX		
PD	16-MAY-2002.	
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PF	02-NOV-2001; 2001WO-US46350.	
XX		
PR	07-NOV-2000; 2000US-245866P.	
XX		
PA	(ANAD-) ANADYS PHARM INC.	

XX Blichko V;
XX
DR WPI: 2002-490082/52.
DR P-PSDB: AAO18000, AAO18001.
XX
PT Novel nucleic acid encoding replication competent recombinant hepatitis
C virus genome useful for screening anti-hepatitis C virus therapeutics
and for vaccine development
XX
PS Claim 6, Page 43-47, 85pp; English.
XX
CC The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication-complement
CC non-infectious, replication-defective infection-component, and
CC replication-defective non-infectious HCV, in gene therapy or gene
CC vaccination targeted to hepatic tissue for treating an animal infected or
CC susceptible to HCV infection and for studying HCV infection and
CC propagation. The present sequence is a clone of a fragment of the HCV
CC genome which encodes the core-neo and NS3 proteinase/helicase proteins.
XX
XX
SQ Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 other;

Query Match 99.9%; Score 7985.6; DB 24; Length 7992;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7988; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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2401 GCGCATCTACAGCCCTACTGTAAGGCGCAAGACACTAAGGTGCCGCTGGCTATGCA 2460
2401 GCGCATCTACAGCCCTACTGTAAGGCGCAAGACACTAAGGTGCCGCTGGCTATGCA 2460
2461 GCGCAAGGGTATTAAGTCTGTCTGTAACCCGCTCGCGCACCTAGTTCGGG 2520
2461 GCGCAAGGGTATTAAGTCTGTCTGTAACCCGCTCGCGCACCTAGTTCGGG 2520
2461 GCGCAAGGGTATTAAGTCTGTCTGTAACCCGCTCGCGCACCTAGTTCGGG 2520
2521 GCGTATATGTCTAAGGACATGATGATGACCCCTAACATCAGAACCGGGGTAAAGACATC 2580
2521 GCGTATATGTCTAAGGACATGATGATGACCCCTAACATCAGAACCGGGGTAAAGACATC 2580
2581 ACCAGGGGTGCCCCCATACGTAAGTCTGACCTATGCAAGTTCCTTGGCGAGGGGTGCG 2640
2581 ACCAGGGGTGCCCCCATACGTAAGTCTGACCTATGCAAGTTCCTTGGCGAGGGGTGCG 2640
2641 TCTGGGGGGGCTATGACATCATATATGATGATGATGATGATGATGATGATGATGATG 2700
2641 TCTGGGGGGGCTATGACATCATATATGATGATGATGATGATGATGATGATGATGATG 2700
2701 ATCTGAGGATGAGAGAGTCTGAGCAAGCGAGAGAGGCTGAGAGCGGCACTGCTGCTG 2760
2701 ATCTGAGGATGAGAGAGTCTGAGCAAGCGAGAGAGGCTGAGAGCGGCACTGCTGCTG 2760
2761 CTGCGCACCGCTACGCGCTCGGGGATGCTACCGCTGCAACATGCAACATGAGAGAGT 2820
2761 CTGCGCACCGCTACGCGCTCGGGGATGCTACCGCTGCAACATGCAACATGAGAGAGT 2820

2761 CTGCGCACCGCTACGCGCTCGGGGATGCTACCGCTGCAACATGCAACATGAGAGAGT 2820
2821 GCTCTGTCAGCACTGGAGAAATCCCTTTATGGCAAGCCATCCCATGAGACATC 2880
2821 GCTCTGTCAGCACTGGAGAAATCCCTTTATGGCAAGCCATCCCATGAGACATC 2880
2881 AAGGGGGGAGGACCTCATTTTCTGCCATTTCCAGAGAAATGTGATAGTCTGCGCGG 2940
2881 AAGGGGGGAGGACCTCATTTTCTGCCATTTCCAGAGAAATGTGATAGTCTGCGCGG 2940
2941 AAGCTGCGGCTCGGACCTCATCTGTAGCATATTTACGGGGGCTTATGATTCGTC 3000
2941 AAGCTGCGGCTCGGACCTCATCTGTAGCATATTTACGGGGGCTTATGATTCGTC 3000
2941 AAGCTGCGGCTCGGACCTCATCTGTAGCATATTTACGGGGGCTTATGATTCGTC 3000
3001 ATACCACTAGCGAGACGTCATTTGCTAGCAACGAGGCTCTAATGACGGGCTTTACC 3060
3001 ATACCACTAGCGAGACGTCATTTGCTAGCAACGAGGCTCTAATGACGGGCTTTACC 3060
3061 GGCATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
3061 GGCATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
3061 GGCATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
3121 CTGAGCCGACCTTCAACCTTTGAGACGACGACGCTGCCAACAGCGGCTGACGCTGCG 3180
3121 CTGAGCCGACCTTCAACCTTTGAGACGACGACGCTGCCAACAGCGGCTGACGCTGCG 3180
3181 CAGGCGCGAGGAGGACTGTAGGGGAGAGTGGGCTTTACAGTTTGTGATCTCAGCA 3240
3181 CAGGCGCGAGGAGGACTGTAGGGGAGAGTGGGCTTTACAGTTTGTGATCTCAGCA 3240
3181 CAGGCGCGAGGAGGACTGTAGGGGAGAGTGGGCTTTACAGTTTGTGATCTCAGCA 3240
3241 GAAGGCGGCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
3241 GAAGGCGGCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
3241 GAAGGCGGCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
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3301 GCTTGTACGAGCTACGCGCGCGGAGACCTGATGATGATGATGATGATGATGATGATG 3360
3361 CAGGCTGCGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3420
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3421 ACCCATAGAGCGCCATTTCTTGTCCAGAGTAAAGGAGGAGGAGGAGGAGGAGGAGG 3480
3421 ACCCATAGAGCGCCATTTCTTGTCCAGAGTAAAGGAGGAGGAGGAGGAGGAGGAGG 3480
3481 CTGCTAGCATACGAGGCTAGCGGTGTGGCGAGGGCTAGGGCTCACCTCATGCTGGAC 3540
3481 CTGCTAGCATACGAGGCTAGCGGTGTGGCGAGGGCTAGGGCTCACCTCATGCTGGAC 3540
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3601 TATAGGCTGGAGGAGGCTTCAAAAGAGGATCTACACAGGAGGAGGAGGAGGAGGAGG 3660
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QY 3901 GAACATTCACACAGAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCT 3960
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DB 4021 TGGAAATTCATCAGCGGGATACATATTTAGAGGCTTGCTGCTGCTGCGCAACCC 4080
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DB 4081 GCGATAGCATCATGATGGCATTCACAGCTCTATCACAGCCGCTCAGCAGCCAACT 4140
QY 4141 ACCCTCGCTTTAACATCCTGSGGGGATGGGTGGCGCCCAACTTGCTCCCGAGGCT 4200
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QY 4261 AAGGTGCTTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTGCTGGCC 4320
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DB 4321 TTTAAGGTATGAGGCGCGGCAGATGCCCTCCACGAGAGCTTGCTAACCTACTGCTGCT 4380
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DB 4381 ATCCCTCCGCTGCGCCCTAGTCGTCGCGGAGCTGCTGGCGAGCATACTGCTGCGGAC 4440
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DB 4441 GTGGGCGCAGGAGGAGGAGCTGTGAGTGAACCGGCTGATAGCTTGGCTTGGCGG 4500
QY 4501 GGTAAACAGGTCGCGCCGAGCATGTGCTGAGAGGAGCGCTGAGCAGGTGCTGCT 4560
DB 4501 GGTAAACAGGTCGCGCCGAGCATGTGCTGAGAGGAGCGCTGAGCAGGTGCTGCT 4560
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DB 4801 CAACACACCTGCGCATGTGAGAGCAGATCACGAGCATGTGAAAGAGCTTCATGAGG 4860
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DB 5821 ACGGCTCTCTGACAGGCTTCCGAGAGGAGGAGGAGGAGTTCGAGCTTGTGAGTAC 5880
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DB 5941 TCTACCTAGCAGAGAGCTAGTGAAGAGCTGCTGCTGCTGAGTCTTACACATGG 6000
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Db 7921 TAGCTGGAAGAGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 7980
Qy 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 2
AAL47281 standard; DNA; 7992 bp.
AAL47281:
30-AUG-2002 (first entry)
Hepatitis C virus sub-genomic replicon recombinant clone HCVB24.
Hepatitis: HCV; core-neo; NS3 protease/helicase; vaccine; diagnosis;
viral; hepatitis; gene therapy; anti-viral; gene; ds.
Hepatitis C virus.
OS
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XX WO00238793-A2.
PN 16-MAY-2002.
XX 02-NOV-2001: 2001WO-US46350.
XX 07-NOV-2000: 2000US-245866P.
XX (ANAD-) ANADYS PHARM INC.
XX Bichko V.
XX WPI: 2002-49082/52.
XX Novel nucleic acid encoding replication competent recombinant hepatitis
PT C virus genome useful for screening anti-hepatitis C virus therapeutics
PT and for vaccine development
XX Claim 11: Page 70-75; 85pp; English.
XX The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication-complement
CC non-infectious, replication-defective infection-component, and
CC replication-defective non-infectious HCV, in gene therapy or gene
CC vaccination targeted to hepatic tissue for treating an animal infected or
CC susceptible to HCV infection and for studying HCV infection and
CC propagation. The present sequence is a clone of a fragment of the HCV
CC genome designated HCV824.
XX
SO Sequence 7992 BP; 1648 A; 2369 C; 2242 G; 1733 T; 0 other:
Query Match 99.98; Score 7984; DB 24; Length 7992;
Best Local Similarity 99.98; Prid. No. 0;
Matches 7987; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 GCACGCCCCCATGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60
DB 1 GCACGCCCCCATGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60
OY 61 TCTTCACGCAAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGCAAGCCCTCCAGGAC 120
DB 61 TCTTCACGCAAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGCAAGCCCTCCAGGAC 120
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DB 121 CCCCCCTCCGGGAGAGCAATAGTGTCTGGGAAACCGGTGATACACGGAAATCCAG 180
OY 181 GACGACGGGTCTTCTTGGATACACCCGCTCAATGCTGAGATTTGGGCTGCCCC 240
DB 181 GACGACGGGTCTTCTTGGATACACCCGCTCAATGCTGAGATTTGGGCTGCCCC 240
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DB 241 GGGAACTGTACGCGAGTACTGTGGGTGGCGAAAGCGCTTGGTGGTACTGCTGATAG 300
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DB 301 GTGCTTGGAGTGGCCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGAAATCTAAG 360
OY 361 CTCAGAGAAAAACCAAGGCGCGCATGATTGAACAAGATGGATTGACGAGGTTCTC 420
DB 361 CTCAGAGAAAAACCAAGGCGCGCATGATTGAACAAGATGGATTGACGAGGTTCTC 420
OY 421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGGGCAACAGACAAATGGCTGCT 480
DB 421 CGGCGCTTGGGTGAGAGGCTATTGGCTATGACTGGGCAACAGACAAATGGCTGCT 480

OY 481 CTGATCCGCGGCTGTCCGGCTGTACGCGCAGGGGCGCCGGTCTTTTGTACAGACCG 540
DB 481 CTGATCCGCGGCTGTCCGGCTGTACGCGCAGGGGCGCCGGTCTTTTGTACAGACCG 540
OY 541 ACCTGTCCGGTCCCTGAAATGAATGACGAGCAGGCGGCTATGCTGTGCGCA 600
DB 541 ACCTGTCCGGTCCCTGAAATGAATGACGAGCAGGCGGCTATGCTGTGCGCA 600
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DB 601 CGACGGGCGTCTTCCGAGAGTGTGCTGAGCTGTGCTACTGAAGCGGAGGAGCTGCG 660
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DB 721 AAGTATCCATCATGCTGTGATGCAATGCGGCGCTGATAGCTTATCCGCTACTGCTCC 780
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DB 781 CATTGACACCAAGGAAACATCGCATGAGCAGACGATCTGATGGAAGCGGCTC 840
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DB 841 TTGTGATCAGATGATCTGAGAGAGACATCAGGGGCTCGGCGAGCAGCTGTG 900
OY 901 CCAAGGCTCAAGGCGCGCATGTCGCGAGGAGAGATCTGCTGTGACCATGAGGATGCT 960
DB 901 CCAAGGCTCAAGGCGCGCATGTCGCGAGGAGAGATCTGCTGTGACCATGAGGATGCT 960
OY 961 GCTTGGCGGATATCATGCTGTGAGAAATGCGCGCTTCTGAGTTCANCGCTGTGCGCG 1020
DB 961 GCTTGGCGGATATCATGCTGTGAGAAATGCGCGCTTCTGAGTTCANCGCTGTGCGCG 1020
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DB 1021 TGGGTGTGCGGAGCCGCTATCAGAGACATAGCGTTGAGTACCGGTATTTGCTGAGAGC 1080
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DB 1081 TTGCGCGGATGAGGCTGACCGCTTCTGCTGTGCTTTAGCGTATCCGCGCTCCGAGTGGC 1140
OY 1141 AGGCGATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACGAGCACAAGC 1200
DB 1141 AGGCGATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACGAGCACAAGC 1200
OY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAGCTTACTGGC 1260
DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAAGCTTACTGGC 1260
OY 1261 CGAAGCGGCTTGAATAGGCGGAGTGTGCTTGTGTATATGATATTTCCACCATATG 1320
DB 1261 CGAAGCGGCTTGAATAGGCGGAGTGTGCTTGTGTATATGATATTTCCACCATATG 1320
OY 1321 CCGTCTTTTGGCAATGTGAGGCGCCGGAACCTGTGCTCTTCTTGTGAGAGATTTCT 1380
DB 1321 CCGTCTTTTGGCAATGTGAGGCGCCGGAACCTGTGCTCTTCTTGTGAGAGATTTCT 1380
OY 1381 AGGGGTCTTCCCTCTCGCGCAAGGAAATGCAAGGTTGTGATGTGCGAAGAGA 1440
DB 1381 AGGGGTCTTCCCTCTCGCGCAAGGAAATGCAAGGTTGTGATGTGCGAAGAGA 1440
OY 1441 GTTCTCTGGAAGCTTCTGAAAGCAAAACGCTGTGTAGCGACCTTTGACGAGCGG 1500
DB 1441 GTTCTCTGGAAGCTTCTGAAAGCAAAACGCTGTGTAGCGACCTTTGACGAGCGG 1500
OY 1501 AACCCCGCACTGCGGACAGTGTCTCTGCGGCAAAAGCGAGGTGATTAAGTACACT 1560
DB 1501 AACCCCGCACTGCGGACAGTGTCTCTGCGGCAAAAGCGAGGTGATTAAGTACACT 1560


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Db 3721 GTCTAGCAGCTCTGCGCGCATTTGCTGACAAACAGGACAGTGTGTCATTTGTGGCAGG 3780
Qy 3781 ATCATTTTTCGGGAAGGCGGCCATCATTTCCCGACAGGAGAGTCCTTTACCGGAGATTC 3840
Db 3781 ATCATTTTTCGGGAAGGCGGCCATCATTTCCCGACAGGAGAGTCCTTTACCGGAGATTC 3840
Qy 3841 GATGAGATGAGAGATGCGCCTCACACCTCCCTTACATGCAAGAGGATGCAACTCGCC 3900
Db 3841 GATGAGATGAGAGATGCGCCTCACACCTCCCTTACATGCAAGAGGATGCAACTCGCC 3900
Qy 3901 GAACAAATTCAACAGAGGCAATCGGGTTGCTGCAAAAGCGCCACCAAGCAAGCGGAGCT 3960
Db 3901 GAACAAATTCAACAGAGGCAATCGGGTTGCTGCAAAAGCGCCACCAAGCAAGCGGAGCT 3960
Qy 3961 GCTGCTCCGCTGGTGAATCCCAAGTGGCGGACCTCGAAGCCTTCTGCGGCAACATATG 4020
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Db 4141 ACCCTCCTGTTTAACATCCTGGGGGATGGGTGGCCGCCAACTTGCTCTCCACGCGCT 4200
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Db 4261 AAGGTGCTTGATATTTTGGCAGTTATGAGCAGGGGTTGAGCGCGCTGCTGGCC 4320
Qy 4321 TTTAAGTCAATGACCGCGGAGATGCGCTCCACGAGAGACTGGCTAATCCTTACCTCTCT 4380
Db 4321 TTTAAGTCAATGACCGCGGAGATGCGCTCCACGAGAGACTGGCTAATCCTTACCTCTCT 4380
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Db 4621 GAGAGTGTCTCAAGGCACTCTCGGCTGTGCTGAAGAGATGTTGGATGATGATGAC 4680
Qy 4681 ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGAGTCTCTGCGGATTTGCCGGGA 4740
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Db 4921 ACCAGGCGCCCTGACGCGCCTCCCGCGCCAAATTTATCTAGGGGCTGTGGCGGGTG 4980
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Db 5041 ACCACTGACACGTAAGTGTCCGCTGTGAGCTTCGCGCCCGCGAATTTCTTACAGAGTG 5100
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Db 6241 GAGGCGGTAGGCTGAGCGGCGGCGACATGCGGAGATCTAAATTTGGCTATGGGGCAAG 6300
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QY 7621 TTATCAGCTGTGTTCTGTCTGCTTACAGCGGAGGAGACATATATACAGCCTGTCTGT 7680
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QY 7861 TTTTCTCTTTTCTTTCTTTTCTTTCTTTCTTTGCTGCTCATCTTACGCTACGCGC 7920
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QY 7921 TAGCTGAAGAGTCCGAGACGCTTACGAGCAGAGAGTGTGATAGTGGCTCTCTGCG 7980
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Db 7921 TAGCTGAAGAGTCCGAGACGCTTACGAGCAGAGAGTGTGATAGTGGCTCTCTGCG 7980
QY 7981 AGATCAAGTACT 7992
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Db 7981 AGATCAAGTACT 7992
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RESULT 3
AAA98968
ID AAA98968 standard; DNA; 7989 BP.
XX
AC AAA98968:
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Db 1441 GTTCCCTGAGAGCTTCTTGAAGACAACAACGTCGTAGGACCTTTGCGAGGACGG 1500
Qy 1501 AACCCCCACCTGGGAGAGGTGCTCTGGGCCCCAAAAGCCAGCTGTAAGATACACT 1560
Db 1501 AACCCCCACCTGGGAGAGGTGCTCTGGGCCCCAAAAGCCAGCTGTAAGATACACT 1560
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Qy 1861 AGCCTACAGGCGGAGACAGGAACAGAGTGAAGGGGAGGTCCAGTGTCTCCACGCCA 1920
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Qy 1921 ACACATCTTCTCTGGCGACGTGCTGATGAGCGGTGTGTGAGACGTGTATCATGATGCC 1980
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Qy 1981 GGGTCAAGAGCCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2040
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Db 2041 CAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
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Db 2461 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520
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Db 2581 ACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Qy 2641 TCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2700
Db 2641 TCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2700
Qy 2701 ATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
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Db 2821 GCTCTGTCCAGCAGTGAAGAAATCCCTTTTATGSCAAAGGCAATCCCATGAGACCATC 2880
Qy 2881 AAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2940
Db 2881 AAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2940
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Db 2941 AAGCTGTCCGCTCGGAGTCAATGCTGTAGATATACCGGGGCTGTGATTCGCTG 3000
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Qy 3541 CAATGTGAGAGTGTCTCATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3600
Db 3541 CAATGTGAGAGTGTCTCATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3600
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QY	3601	TATAGGCGGGAGGCGCTGAAAACGAGCTAGTACACAGACACCCCAATACCAATATCATC	3660
Db	3601	TATAGGCGGGAGGCGCTTCAAAACGAGGTTACTACACACCCCAATACCAATATCATC	3660
QY	3661	ATGCGATGCATGTGCGGTGACCTGAGAGTGTGTCACAGACACCTGGGTGCTGTAGCGGA	3720
Db	3661	ATGGCATCATGTGCGGTGACCTGAGAGTGTGTCACAGACACCTGGGTGCTGTAGCGGA	3720
QY	3721	GTCCTAGAGCTCTGGCGCGCTATTGCTGTGACACAGGCAAGCGTGGTATGGGACAG	3780
Db	3721	GTCCTAGAGCTCTGGCGCGCTATTGCTGTGACACAGGCAAGCGTGGTATGGGACAG	3780
QY	3781	ATCATCTGTCCGGAAGGCGCGCCATTCATCCGACAGGGAAGTCTTTACCGGGAGTTC	3840
Db	3781	ATCATCTGTCCGGAAGGCGCGCCATTCATCCGACAGGGAAGTCTTTACCGGGAGTTC	3840
QY	3841	GATGAGATGGAAGAGTGGGCTCACACCTCCCTTACATGACAGGGAATGACAGCTGGC	3900
Db	3841	GATGAGATGGAAGAGTGGGCTCACACCTCCCTTACATGACAGGGAATGACAGCTGGC	3900
QY	3901	GAAACATTTCAACAGAAAGCATGGGTGTGCAACACGCCAACAGCAAGGGAAGGT	3960
Db	3901	GAAACATTTCAACAGAAAGCATGGGTGTGCAACACGCCAACAGCAAGGGAAGGT	3960
QY	3961	GCTGCTCCCGGTGTGGAATCCAGTGGGAGCCTCGAAGCCTTCTGGGCGAAGCATATG	4020
Db	3961	GCTGCTCCCGGTGTGGAATCCAGTGGGAGCCTCGAAGCCTTCTGGGCGAAGCATATG	4020
QY	4021	TGGATTTTCATCAGGGGATACATATTATAGCAGGCTTGTCACATCTGCTGGCAACCC	4080
Db	4021	TGGATTTTCATCAGGGGATACATATTATAGCAGGCTTGTCACATCTGCTGGCAACCC	4080
QY	4081	GCGATAGCATCACTGATGCAATTCACAGCCCTATACACAGCCCGCTACACACCAACAT	4140
Db	4081	GCGATAGCATCACTGATGCAATTCACAGCCCTATACACAGCCCGCTACACACCAACAT	4140
QY	4141	ACCTTCCTGTTTAACATCCTGGGGGAGTGGGTGGCCCGCACTTGCTCCCAAGGCT	4200
Db	4141	ACCTTCCTGTTTAACATCCTGGGGGAGTGGGTGGCCCGCACTTGCTCCCAAGGCT	4200
QY	4201	GCTTCCTGTTTCGTAGGGCGCGGCATCGCTGAGCGGCTGTGGCAGCATAGGCTTGGG	4260
Db	4201	GCTTCCTGTTTCGTAGGGCGCGGCATCGCTGAGCGGCTGTGGCAGCATAGGCTTGGG	4260
QY	4261	AAGGTCCTGTGTGATTTTGGCAGGTTATGAGAGGGGGTGGAGGGGCGCTGTGGCC	4320
Db	4261	AAGGTCCTGTGTGATTTTGGCAGGTTATGAGAGGGGGTGGAGGGGCGCTGTGGCC	4320
QY	4321	TTTAAAGTCATAGCGGGAGATGCGCTTCAACCGAGACCTGGTTAACCTACTCCAGCT	4380
Db	4321	TTTAAAGTCATAGCGGGAGATGCGCTTCAACCGAGACCTGGTTAACCTACTCCAGCT	4380
QY	4381	ATCTCTCTCCCTGCGCCCTAGTGTGCGGGGTGTGTGCGCAGCGATACTGCTCGGAC	4440
Db	4381	ATCTCTCTCCCTGCGCCCTAGTGTGCGGGGTGTGTGCGCAGCGATACTGCTCGGAC	4440
QY	4441	GTGGGCGCCAGGGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGGCTTGGCTCGGG	4500
Db	4441	GTGGGCGCCAGGGGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGGCTTGGCTCGGG	4500
QY	4501	GGTAAACCAAGTCTCCCCACGACATATGTGCTGAGAGCGAGCGCTGACGACGTGTACT	4560
Db	4501	GGTAAACCAAGTCTCCCCACGACATATGTGCTGAGAGCGAGCGCTGACGACGTGTACT	4560
QY	4561	CAGATCTCTTATGTCTTACATCACTCAGTGTGTAAGAGGCTTCAACCAATGATATAC	4620
Db	4561	CAGATCTCTTATGTCTTACATCACTCAGTGTGTAAGAGGCTTCAACCAATGATATAC	4620
QY	4621	GAGGATGTGTCAACGCGCATGCTCGGCTGTGGCTAAGAGATGTTGGATTGGATATGC	4680
Db	4621	GAGGATGTGTCAACGCGCATGCTCGGCTGTGGCTAAGAGATGTTGGATTGGATATGC	4680
QY	4681	ACGGTGTACTGATTTCAAGACCTGGGTCACAGTCCAAAGCTCTGCGCGATTCGCGGA	4740
Db	4681	ACGGTGTACTGATTTCAAGACCTGGGTCACAGTCCAAAGCTCTGCGCGATTCGCGGA	4740
QY	4741	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGGGGCGACGGCATCATG	4800
Db	4741	GTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGGGGCGACGGCATCATG	4800
QY	4801	CAAAACCACTGCCATGTGGAGCAGATCCCGCATGTGAAAAAAGGTTCCATGAG	4860
Db	4801	CAAAACCACTGCCATGTGGAGCAGATCCCGCATGTGAAAAAAGGTTCCATGAG	4860
QY	4861	ATCGTGGGCGCTAGGACTGTAGTAAACGTGCGATGAGAACATTTCCCATTAACGCTAC	4920
Db	4861	ATCGTGGGCGCTAGGACTGTAGTAAACGTGCGATGAGAACATTTCCCATTAACGCTAC	4920
QY	4921	ACCAGGGGCGCTGACGCGCTCCCGGCGCAATTTATCTAGGCGCTGTGGCGGGT	4980
Db	4921	ACCAGGGGCGCTGACGCGCTCCCGGCGCAATTTATCTAGGCGCTGTGGCGGGT	4980
QY	4981	GCTGCTGAGAGATACGTGAGGTTACGCGGATGGGGATTTCACACTACGTACGCGCATG	5040
Db	4981	GCTGCTGAGAGATACGTGAGGTTACGCGGATGGGGATTTCACACTACGTACGCGCATG	5040
QY	5041	ACCACTGACAAAGTAAAGTCCCGTGTAGGTTCCGGCCCCGCAATCTTACAGAAAGT	5100
Db	5041	ACCACTGACAAAGTAAAGTCCCGTGTAGGTTCCGGCCCCGCAATCTTACAGAAAGT	5100
QY	5101	GATGGGATGGCGGTTCCACAGGTACGCTCACAGGTGCAAAACCCCTCTACGGGAGAGTC	5160
Db	5101	GATGGGATGGCGGTTCCACAGGTACGCTCACAGGTGCAAAACCCCTCTACGGGAGAGTC	5160
QY	5161	ACATTCCTGTGTGGGCTAATCAATACCTGTTGGTTCACAGCTCCCATGGAGCCGAA	5220
Db	5161	ACATTCCTGTGTGGGCTAATCAATACCTGTTGGTTCACAGCTCCCATGGAGCCGAA	5220
QY	5221	CCGAGCTGAGCACTGCTACTTCATGCTCACAGCCGCCCTCCCATTTACGGCGAGAGC	5280
Db	5221	CCGAGCTGAGCACTGCTACTTCATGCTCACAGCCGCCCTCCCATTTACGGCGAGAGC	5280
QY	5281	GCTAAGCGTAGGCTGCGCCAGGGGATCTCCCGCTCTTGGGCAAGTCAACGTACAGCAG	5340
Db	5281	GCTAAGCGTAGGCTGCGCCAGGGGATCTCCCGCTCTTGGGCAAGTCAACGTACAGCAG	5340
QY	5341	CTGTCTGCGCCTTCTTGAAGCAACATGCACTACCCCTCATGTGATCCCGCGAGCTGAC	5400
Db	5341	CTGTCTGCGCCTTCTTGAAGCAACATGCACTACCCCTCATGTGATCCCGCGAGCTGAC	5400
QY	5401	CTCATGAGAGCCAACTCTCTGGCGGAGGAGGATGGGCGGGAATCACCGCGGTGAG	5460
Db	5401	CTCATGAGAGCCAACTCTCTGGCGGAGGAGGATGGGCGGGAATCACCGCGGTGAG	5460
QY	5461	TCAGAAATTAAGTGTATTTTGGACGTTTTCGAGCGGCTCCAAAGCGGAGAGATGAG	5520
Db	5461	TCAGAAATTAAGTGTATTTTGGACGTTTTCGAGCGGCTCCAAAGCGGAGAGATGAG	5520

Db	5761	GAATGTCGCCAACAAGACCTTGGGACGTCCGAATGTGCGCCGTCGACAGCGGGACGGCA	5820
Qy	5821	ACGGGCTCTCTCTGACCAGCCCTTCGCACAGCGGCACGCGGGATCTCCAGCTTGAATGCTAC	5880
Db	5821	ACGGGCTCTCTCTCTGACCAGCCCTTCGCACAGCGGCACGCGGGATCTCCAGCTTGAATGCTAC	5880
Qy	5881	TCCTCCATGCGCCCCCTTGTAGGGGGAGCGCGGGGATGCCGATCTTCAGCGAGGGTCTTGG	5940
Db	5881	TCCTCCATGCGCCCCCTTGTAGGGGGAGCGCGGGGATGCCGATCTTCAGCGAGGGTCTTGG	5940
Qy	5941	TCTACCGTAAAGCAGAGGCTAGTAGAGCGTCGTCTCTCTCTGATGTCTCTACACATGG	6000
Db	5941	TCCTACCGTAAAGCAGAGGCTAGTAGAGCGTCGTCTCTCTCTGATGTCTCTACACATGG	6000
Qy	6001	ACAGGGCCCCGATACACGGCATATGCGGTGGGGAGAAACCAAGTCGCCCATTAATGCACCTG	6060
Db	6001	ACAGGGCCCCGATACACGGCATATGCGGTGGGGAGAAACCAAGTCGCCCATTAATGCACCTG	6060
Qy	6061	AGCAACTCTTTGGCTCGGTACCCACAACCTTGATGTGTACAGACTCTGCAGCGCAAGC	6120
Db	6061	AGCAACTCTTTGGCTCGGTACCCACAACCTTGATGTGTACAGACTCTGCAGCGCAAGC	6120
Qy	6121	CTGCGGAGAGAAGGTCACACTTTGACACACTGCGAGTCTCGAGACCACTACCGGGAC	6180
Db	6121	CTGCGGAGAGAAGGTCACACTTTGACACACTGCGAGTCTCGAGACCACTACCGGGAC	6180
Qy	6181	GTCGTCACAGGATGAAGAGGCGTCCACAGTTAAGGGCTAAACTCTATCCGTGGAG	6240
Db	6181	GTCGTCACAGGATGAAGAGGCGTCCACAGTTAAGGGCTAAACTCTATCCGTGGAG	6240
Qy	6241	GAAGCTGTGTAAGCTGACGCCCCCACAATTGGCCAGATCTAAATTTGGCTATGGGGCAAG	6300
Db	6241	GAAGCTGTGTAAGCTGACGCCCCCACAATTGGCCAGATCTAAATTTGGCTATGGGGCAAG	6300
Qy	6301	GACGTCGGGAACCTATCCACCAAGGGCGTTAACCAATCGCTCCGTGTGGAAGACTGTG	6360
Db	6301	GACGTCGGGAACCTATCCACCAAGGGCGTTAACCAATCGCTCCGTGTGGAAGACTGTG	6360
Qy	6361	CTGGAAGACACTGAGACCAACATTTGACACACCACATATGGCAAAAATAGAGTTTCTGC	6420
Db	6361	CTGGAAGACACTGAGACCAACATTTGACACACCACATATGGCAAAAATAGAGTTTCTGC	6420
Qy	6421	GTCACACAGAGAGAGGGGGCCCCAGACCAAGTCGCGCTATGTATTCACAGATTGGGG	6480
Db	6421	GTCACACAGAGAGAGGGGGCCCCAGACCAAGTCGCGCTATGTATTCACAGATTGGGG	6480
Qy	6481	GTTCTGTGTGTCGAGAAAATGGCCCTTTACGATGTGTCTCCACCCCTCCTCAGCCGTG	6540
Db	6481	GTTCTGTGTGTCGAGAAAATGGCCCTTTACGATGTGTCTCCACCCCTCCTCAGCCGTG	6540
Qy	6541	ATGGGCTCTTATACGATTCGAATCTCTCTCTGAGACACCGGGTGGAGTTCCTGGTGAAT	6600
Db	6541	ATGGGCTCTTATACGATTCGAATCTCTCTCTGAGACACCGGGTGGAGTTCCTGGTGAAT	6600
Qy	6601	GCGTGAAGAGGAGAAATGGCCATATGGCTTGGCTGCAATAGACACCGCGTGTTTGACTCA	6660
Db	6601	GCGTGAAGAGGAGAAATGGCCATATGGCTTGGCTGCAATAGACACCGCGTGTTTGACTCA	6660
Qy	6661	ACGGTCTAGTAATGACATCCGTGTGTGAGAGTCAATCTACCAATGTGTACTTGGCC	6720
Db	6661	ACGGTCTAGTAATGACATCCGTGTGTGAGAGTCAATCTACCAATGTGTACTTGGCC	6720
Qy	6721	CGCGAAGCAGACGAGGCGCATATAGGTCCCTACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Db	6721	CGCGAAGCAGACGAGGCGCATATAGGTCCCTACAGAGCGGCTTTACATCGGGGGCCCCCTG	6780
Qy	6781	ACTAATTCTAAAGGCGACAACCTGCGGTATGCGCGGTGCGCGCGAGCGGTACTGACG	6840
Db	6781	ACTAATTCTAAAGGCGACAACCTGCGGTATGCGCGGTGCGCGCGAGCGGTACTGACG	6840
Qy	6841	ACCACTCGGGTAATACCTCACAATGTACTTGAAGGCGCTCGGCGCTGTGAGACTGTG	6900
Db	6841	ACCACTCGGGTAATACCTCACAATGTACTTGAAGGCGCTCGGCGCTGTGAGACTGTG	6900

QY	6901	AAATCTCAGSAGACTGCACAGATGCTGCTGATATGCGSAGAGSAGACACTTGTGCTATCTGTGAAGC	6960
Db	6901	AAAGTCCAGSAGACTGCACAGATGCTGATATGCGSAGAGSAGACACTTGTGCTATCTGTGAAGC	6960
QY	6961	GGCGGGAGCCCAAGAGAGACGAGGCGAGCCCTTACAGSAGGCTATGACTAGATAC	7020
Db	6961	GGCGGGAGCCCAAGAGAGACGAGGCGAGCCCTTACAGSAGGCTATGACTAGATAC	7020
QY	7021	TCCTCCCCCCTTGGGAGCCCGGCTCAAAACCAATACAGACTTGGAGTTGATTAACATCATGC	7080
Db	7021	TCCTCCCCCCTTGGGAGCCCGGCTCAAAACCAATATCAGACTTGGAGTTGATTAACATCATGC	7080
QY	7081	TCCTCCCATGTGTCAGTGCGGCGACGATGCATGTGGCAAAAGGTTGATATCTCACCCGT	7140
Db	7081	TCCTCCCATGTGTCAGTGCGGCGACGATGCATGTGGCAAAAGGTTGATATCTCACCCGT	7140
QY	7141	GACCCCAACACCCCCCTTGGGCGGGGTGTGGTGGAGACAGCTAGACACATCCAGTCAT	7200
Db	7141	GACCCCAACACCCCCCTTGGGCGGGGTGTGGTGGAGACAGCTAGACACATCCAGTCAT	7200
QY	7201	TCCTGGCTAGGCAACATCATCATGATATGCGCCACCTTGTGGGCAAGATATCTCTATG	7260
Db	7201	TCCTGGCTAGGCAACATCATCATGATATGCGCCACCTTGTGGGCAAGATATCTCTATG	7260
QY	7261	ACTATTTCTTCCTCATCCTCTTGTAGTTCAGGAACAATCTGAATAAGCCCTAGATTGTCAG	7320
Db	7261	ACTATTTCTTCCTCATCCTCTTGTAGTTCAGGAACAATCTGAATAAGCCCTAGATTGTCAG	7320
QY	7321	ATCTACGGGGGCTGTACTCTCATTTGAGCCACTTGAACCTACATCTATTCAACGACTC	7380
Db	7321	ATCTACGGGGGCTGTACTCTCATTTGAGCCACTTGAACCTACATCTATTCAACGACTC	7380
QY	7381	CATGGCCCTTACCGATTTTACTCCATTCAGTACTCTCCAGSAGATCAATAGGGTGGCT	7440
Db	7381	CATGGCCCTTACCGATTTTACTCCATTCAGTACTCTCCAGSAGATCAATAGGGTGGCT	7440
QY	7441	TCATGCTCAGGAACCTTGGGGATACCGCCCTTGTGCAGTCTGAGACATCTGGGGCCAGAGT	7500
Db	7441	TCATGCTCAGGAACCTTGGGGATACCGCCCTTGTGCAGTCTGAGACATCTGGGGCCAGAGT	7500
QY	7501	GTCGCGCTTAGGCTACTGTCTCCACGAGGGGGAGGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
Db	7501	GTCGCGCGTTAGGCTACTGTCTCCACGAGGGGGAGGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
QY	7561	AACTGGGCAGTAAAGSAGCAAGCTCAAACTACTCCAAATCCCGGCTGCGCCAGTTGGAT	7620
Db	7561	AACTGGGCAGTAAAGSAGCAAGCTCAAACTACTCCAAATCCCGGCTGCGCCAGTTGGAT	7620
QY	7621	TTATTCACAGCTGTTCTGTGTGTATTACAGCGGGGGAGACATATATCACAGCCTGTCTCTGT	7680
Db	7621	TTATTCACAGCTGTTCTGTGTGTATTACAGCGGGGGAGACATATATCACAGCCTGTCTCTGT	7680
QY	7681	GGCCACACCCGCTGTTCAATGATGAGTGGCTACTCTTACTTTCTGTAGGGGTAGGCACTCAT	7740
Db	7681	GGCCACACCCGCTGTTCAATGATGAGTGGCTACTCTTACTTTCTGTAGGGGTAGGCACTCAT	7740
QY	7741	CTATCTCACCACCAACCATGATAGCGGGAGCTAAACACTCCAGGCCAATATAGGCCATCTGTTTT	7800
Db	7741	CTATCTCACCACCAACCATGATAGCGGGAGCTAAACACTCCAGGCCAATATAGGCCAATCTGTTTT	7800
QY	7801	TTTCGCTTTTCTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	7801	TTTCGCTTTTCTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
QY	7861	TTTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	7861	TTTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
QY	7921	TAGGCTGAAGAGTCGAGSAGCGCTTGACGACGAGAGTGGTGAATAGGCTCTGTCC	7980
Db	7921	TAGGCTGAAGAGTCGAGSAGCGCTTGACGACGAGAGTGGTGAATAGGCTCTGTCC	7980

QY	7981	AGATCAAGT	7989
Db	7981	AGATCAAGT	7989

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RESULT 4
AAD25322
ID      AAD25322 standard; cDNA; 7989 BP

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AC	AAD25322;
XX	
DT	12-MAR-2002 (first entry)
XX	

DE Hepatitis C virus (HCV) replBartman/Availi CDNA.

KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 KW gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver
 KW ss.
 KW

OS Hepatitis C virus

FH	Key	Location/Qualifiers
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FT      /product= "HCVreplBartMan polypotein"
FT      7766
FT      /tag= b
FT      /note= "Nucleotide creating Avail site"
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PN W0200189364-A2.

PD 29-NOV-2001

PF 23-MAY-2001; 2001WO-US16822

PR 23-MAY-2000; 2000US-0576989

PA (UNIW) UNIV WASHINGTON.

PI Rice CM, Blight KJ;

DR WPI; 2002-066755/09.

DR P-PSDB; AA615717

PT Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences

PS Claim 44; Page 69-71; 174pp; English.

The invention relates to Hepatitis C virus (HCV) variants which include polynucleotides comprising non-naturally occurring HCV sequence and HCV variants that have a transfection efficiency and ability to survive subpassage greater than HCV that have wild-type polypeptide coding regions. The polynucleotides of the invention are useful for identifying a cell line that is permissive for infection with HCV and detecting replication of HCV in cells of the cell line. They are also useful for testing a compound for anti-viral properties and for inhibiting HCV infection. They are also useful for the generation of defined HCV virus stocks to develop *in vitro* and *in vivo* assays for virus neutralisation, attachment, penetration and entry, structure/function studies on HCV proteins and RNA elements and identification of new antiviral targets, a systematic survey of cell culture systems and conditions to identify those that support wild-type and variant HCV RNA replication and particle release, production of adaptive HCV variants capable of more efficient replication in cell culture, production of HCV variants with altered tissue or species tropism, establishment of alternative animal models for inhibitor evaluation including those supporting HCV variant replication, development of cell-free HCV replication assays, production of immunogenic HCV particles for vaccination, engineering of attenuated HCV derivatives as possible vaccine candidates, engineering of attenuated or defective HCV derivatives for expression of

heretofore gene products for gene therapy and vaccine applications
and for utilisation of the HCV glycoproteins for targeted delivery of
therapeutic agents to the liver or other cell types with appropriate
receptors. Vaccine comprising these sequences is useful for inducing
immuno-protection to HCV in a primate. The present sequence is
Hepatitis C virus (HCV) replicon/anti-HCV cDNA.

SQ Sequence 7989 BP; 1647 A; 2369 C; 2242 G; 1731 T; 0 other;

Query Match	99.98;	Score 7981;	DB 24,	Length 7989;
Best Local Similarity	99.98;	Pred. No. 0;		
Matches 7984; Conservative	0;	Mismatches 5;	Inbels 0;	Gaps 0

QY	1	GGGAGGCCCCGAAATGGGGGGGCGACACCTCCACCATAGATACACTCCCGTGGAGAACTACTG	60
Db	1	GCCAGCCCCGATGGGGGGGCGACACTCCACCATAGATACACTCCCGTGGAGAACTACTG	60
QY	61	TCTTCAAGCAGAAAGGCTGTAGSCCATGGCGTTAGTATGAGTGTCGTGCAAGCTCCAGAC	120
Db	61	TCTTCAAGCAGAAAGGCTGTAGSCCATGGCGTTAGTATGAGTGTCGTGCAAGCTCCAGAC	120
QY	121	CCCCCCTCCCGGGAGAGGCATAGTGGTCTGGGGACCGGAGTACCGCGGATTTGCCAG	180
Db	121	CCCCCCTCCCGGGAGAGGCATAGTGGTCTGGGGACCGGAGTACCGCGGATTTGCCAG	180
QY	181	GAGACCGGGTCTCTTCTTTGGATCAACCGCTCAATGCTCGAGATTTTGGGCTGGCCCC	240
Db	181	GAGACCGGGTCTCTTCTTTGGATCAACCGCTCAATGCTCGAGATTTTGGGCTGGCCCC	240
QY	241	GCGAGACGTGTAGCCGAGTGGGTGGGTCGCGAAAGGCTTGTGTACTGCTGATAGG	300
Db	241	GCGAGACGTGTAGCCGAGTGGGTGGGTCGCGAAAGGCTTGTGTACTGCTGATAGG	300
QY	301	GTCGTTGCGAGTGGCCCGGGAGGCTCTGTAGACCGTGTACCATGAGCACGAATCTTAAC	360
Db	301	GTCGTTGCGAGTGGCCCGGGAGGCTCTGTAGACCGTGTACCATGAGCACGAATCTTAAC	360
QY	361	CTCAAGAAACCAAAAGGGCGCCGCATATGATTAACAAAGTGGATTTGACGAGGTTCTC	420
Db	361	CTCAAGAAACCAAAAGGGCGCCGCATATGATTAACAAAGTGGATTTGACGAGGTTCTC	420
QY	421	CGGCGGCTTGGGTGGAGAGGCTATTGCGCTATGACTGGGACACACAGCAATCGGCTGCT	480
Db	421	CGGCGGCTTGGGTGGAGAGGCTATTGCGCTATGACTGGGACACACAGCAATCGGCTGCT	480
QY	481	CTGATGCGCGCGGTGTCCCGGCTGTACAGCGACAGGGCGGCCCGGTTCTTTTGTCAAGACG	540
Db	481	CTGATGCGCGCGGTGTCCCGGCTGTACAGCGACAGGGCGGCCCGGTTCTTTTGTCAAGACG	540
QY	541	ACCTGTCCGCTGCCCTGATGTAACCTGCACGACGACGCGCGGCTATCTGTGGCTGGCCA	600
Db	541	ACCTGTCCGCTGCCCTGATGTAACCTGCACGACGACGCGCGGCTATCTGTGGCTGGCCA	600
QY	601	CGACGGGCGTTCTCTTGGCGAGCTGTGGCTGCAGCGTTGTCACTGAAGCGGAAAGGACTGGC	660
Db	601	CGACGGGCGTTCTCTTGGCGAGCTGTGGCTGCAGCGTTGTCACTGAAGCGGAAAGGACTGGC	660
QY	661	TGCAATTGGCGGAAGTCCCGGGCGAGGATCTCCCTGTCATCTCACTGCTCTCTCGCAGA	720
Db	661	TGCAATTGGCGGAAGTCCCGGGCGAGGATCTCCCTGTCATCTCACTGCTCTCTCGCAGA	720
QY	721	AAGTATCCATCATGAGCTGATGCAATGGGGCGGCTGCATACGCTTGATCCGGCTACTGGC	780
Db	721	AAGTATCCATCATGAGCTGATGCAATGGGGCGGCTGCATACGCTTGATCCGGCTACTGGC	780
QY	781	CATTGCAACCAACAGGAAACATGCAATCGAGGAGAGTACTGGGATGGAGACGCTGTC	840
Db	781	CATTGCAACCAACAGGAAACATGCAATCGAGGAGAGTACTGGGATGGAGACGCTGTC	840
QY	841	TGTGCAATCAGATGATCTGGACGAAGAAGCATCAGGGGCTCGCGCCACGCCAATCTTTCG	900
Db	841	TGTGCAATCAGATGATCTGGACGAAGAAGCATCAGGGGCTCGCGCCACGCCAATCTTTCG	900

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QY 901 CCAGGCTCAAGGCGCGCATGCGGACGCGGAGAGATCTGCTGCTGACCCATGCGGATGCGCT 960
Db 901 CCAGGCTCAAGGCGCGCATGCGGACGCGGAGAGATCTGCTGCTGACCCATGCGGATGCGCT 960
QY 961 GCTTGCGGAATATCATGCTGGAATAATGCGCGCTTTTCTGATTCATATGACTGTGGCGGCG 1020
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QY 1021 TGGGCTGCGGAGCGGCTATCAGAGACATAGCGTTGGCTACCGCTGATATGCTGGAAGAGC 1080
Db 1021 TGGGCTGCGGAGCGGCTATCAGAGACATAGCGTTGGCTACCGCTGATATGCTGGAAGAGC 1080
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Db 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCCTCTCTGAGCAGCATTTCC 1380
QY 1381 AGGGGTCTTTCCCTCTGCGCAAGGAATGCAAGGTCTGTGAATGTGCGAAGGAAGCA 1440
Db 1381 AGGGGTCTTTCCCTCTGCGCAAGGAATGCAAGGTCTGTGAATGTGCGAAGGAAGCA 1440
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Db 1441 GTTCTCTGGAAGCTTCTTGAAGACAACAGTCTGTAGGAGCCCTTTCAGGACGCG 1500
QY 1501 AACCCCCACCTGGGGAAGAGTGCCTCTGCGGCCCAAAAGCCAGCTGATATACCT 1560
Db 1501 AACCCCCACCTGGGGAAGAGTGCCTCTGCGGCCCAAAAGCCAGCTGATATACCT 1560
QY 1561 GCAAGGCGGCGACAACCCAGTGCACGTTGTGAGTTGATATGTTGGAAGAGTCAAA 1620
Db 1561 GCAAGGCGGCGACAACCCAGTGCACGTTGTGAGTTGATATGTTGGAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGATGCCGAGANGTACCCCATTT 1680
Db 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGATGCCGAGANGTACCCCATTT 1680
QY 1681 ATGGGATCGATGCGGCGCTGCGTGCACATGCTTTACATGTTGTTAGTGAAGTTAAA 1740
Db 1681 ATGGGATCGATGCGGCGCTGCGTGCACATGCTTTACATGTTGTTAGTGAAGTTAAA 1740
QY 1741 AAGCTCTAGGCCCCCGGAACACAGGGAGCTGTTTCTTTGAAAAACAGATATACC 1800
Db 1741 AAGCTCTAGGCCCCCGGAACACAGGGAGCTGTTTCTTTGAAAAACAGATATACC 1800
QY 1801 AAGGGGCTTATAGGCGCTACTCCCAACAGAGCGGAGGCTACTTGGCTGATATAGT 1860
Db 1801 AAGGGGCTTATAGGCGCTACTCCCAACAGAGCGGAGGCTACTTGGCTGATATAGT 1860
QY 1861 AGCTTACAGGCGGAGACAGAAACAGAGTGAAGGGGAGGTCCAGATGTCTCCACGCA 1920
Db 1861 AGCTTACAGGCGGAGACAGAAACAGAGTGAAGGGGAGGTCCAGATGTCTCCACGCA 1920
QY 1921 ACACATCTTTCTGCGGAGCTGCTCAATGCGTGTATGAGTGTATCATGAGTGGC 1980
Db 1921 ACACATCTTTCTGCGGAGCTGCTCAATGCGTGTATGAGTGTATCATGAGTGGC 1980
QY 1981 GGCTCAAGAGCCCTTGCGGCGCAAGGGCCCAATCACCACCAATGTGAGC 2040
Db 1981 GGCTCAAGAGCCCTTGCGGCGCAAGGGCCCAATCACCACCAATGTGAGC 2040

QY 2041 CAGGACCTGCTGCGCTGGAAGGCGCGCGCGGCGGCTTCTGACACATGACACTGC 2100
Db 2041 CAGGACCTGCTGCGCTGGAAGGCGCGCGCGGCGGCTTCTGACACATGACACTGC 2100
QY 2101 GGCAGCTCGGACCTTACTTGTGTACAGAGGCATGCCGATCTTCCGCTGCGCGCGG 2160
Db 2101 GGCAGCTCGGACCTTACTTGTGTGTACAGAGGCATGCCGATCTTCCGCTGCGCGCGG 2160
QY 2161 GGCAGAGCAGAGGAGGAGCTACTCTCCAGAGCGGCTGCTACTTGAAGGCTTTGG 2220
Db 2161 GGCAGAGCAGAGGAGGAGCTACTCTCCAGAGCGGCTGCTACTTGAAGGCTTTGG 2220
QY 2221 GCGGCTCCACTGCTCTGCGCGGACGCTGTGGGCATCTTTCGGGCTGCGGTGCG 2280
Db 2221 GCGGCTCCACTGCTCTGCGCGGACGCTGTGGGCATCTTTCGGGCTGCGGTGCG 2280
QY 2281 ACCGAGGAGGTTGGAGGCGGTGACTTGTACCCGCTGAGCTATGGAACCATATG 2340
Db 2281 ACCGAGGAGGTTGGAGGCGGTGACTTGTACCCGCTGAGCTATGGAACCATATG 2340
QY 2341 CCGTCCCGGCTTACAGGACAACCTGCTCCCGCTGCGCGCTACCGCAGACATTCCAGGTG 2400
Db 2341 CCGTCCCGGCTTACAGGACAACCTGCTCCCGCTGCGCGCTACCGCAGACATTCCAGGTG 2400
QY 2401 GCCATCTACACGCCCTACTGCTAGCGGCAAGAGCACTAAGTGGCGGTGCTATGCA 2460
Db 2401 GCCATCTACACGCCCTACTGCTAGCGGCAAGAGCACTAAGTGGCGGTGCTATGCA 2460
QY 2461 GCGCAAGGATATAGGTGCTGCTGAACCCGCTGCGCGCAACCTTACGTTTCGCG 2520
Db 2461 GCGCAAGGATATAGGTGCTGCTGAACCCGCTGCGCGCAACCTTACGTTTCGCG 2520
QY 2521 GCGTATATGCTTAAGGACATGATGACCCCTTAACATCAAGAACCGGGATTAAGACATC 2580
Db 2521 GCGTATATGCTTAAGGACATGATGACCCCTTAACATCAAGAACCGGGATTAAGACATC 2580
QY 2581 ACCACGGGTGCGCCCATACCTACTGACCTATGCACTATGCAAGTTTCTTCCGAGGCTGTGC 2640
Db 2581 ACCACGGGTGCGCCCATACCTACTGACCTATGCACTATGCAAGTTTCTTCCGAGGCTGTGC 2640
QY 2641 TCTGCGGCGGCTATGACATCATATATGATGATAGTCCACTACTGACCTGACCT 2700
Db 2641 TCTGCGGCGGCTATGACATCATATATGATGATAGTCCACTACTGACCTGACCT 2700
QY 2701 ATCTGGGCTAGGCGACAGTCTCTGAGCAAGCGGAGAGCGGTGAGGCGACTGCTG 2760
Db 2701 ATCTGGGCTAGGCGACAGTCTCTGAGCAAGCGGAGAGCGGTGAGGCGACTGCTG 2760
QY 2761 CTGCGCACGCTAGCGCTCTCGGAGTGGTCAACGCTGCCACATCCAAACATCGAGAGTG 2820
Db 2761 CTGCGCACGCTAGCGCTCTCGGAGTGGTCAACGCTGCCACATCCAAACATCGAGAGTG 2820
QY 2821 GCTGCTCGAGCTAGGAGAAATCCCTTTTATGCAAGAGCATCCCATGAGACATC 2880
Db 2821 GCTGCTCGAGCTAGGAGAAATCCCTTTTATGCAAGAGCATCCCATGAGACATC 2880
QY 2881 AAGGGGAGGAGGACCTATTTTCTGCAATTCAGAGAAATGTATGAGCTGCGCGG 2940
Db 2881 AAGGGGAGGAGGACCTATTTTCTGCAATTCAGAGAAATGTATGAGCTGCGCGG 2940
QY 2941 AAGCTGTGCGGCTGAGCTCAATGCTGATATATACGCGGCTTATGATTCGCTC 3000
Db 2941 AAGCTGTGCGGCTGAGCTCAATGCTGATATATACGCGGCTTATGATTCGCTC 3000
QY 3001 ATACCACTAGCGGAGAGCTATTGTCTAGCAACGAGCGCTATATGAGCGCTTACC 3060
Db 3001 ATACCACTAGCGGAGAGCTATTGTCTAGCAACGAGCGCTATATGAGCGCGCTTACC 3060
QY 3061 GCGATTTGACTGATGATGACACTGCAATCATGTGTACCCGAGAGCTGACTGAGC 3120
Db 3061 GCGATTTGACTGATGATGACACTGCAATCATGTGTACCCGAGAGCTGACTGAGC 3120
```

Db 3061 GCGATTTGAGTACAGTATGCAATAATGATGTGACCCAGACAGTGCATTCAGC 3120
QY 3121 CTGGAGCCGACCTTACCATTTAGACAGACGCGTGGCAAAAGCGGGTGTACAGCTCG 3180
Db 3121 CTGGAGCCGACCTTACCATTTAGACAGACGCGTGGCAAAAGCGGGTGTACAGCTCG 3180
QY 3181 CAGCGGCGAGGAGGAGTGTAGGGGAGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGCGAGGAGGAGTGTAGGGGAGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240
QY 3241 GAAGCGCCCTCGGCGATTTGGATTCTCGGCTTCTGTGCGAGTCTTATGACGGGCGTGT 3300
Db 3241 GAAGCGCCCTCGGCGATTTGGATTCTCGGCTTCTGTGCGAGTCTTATGACGGGCGTGT 3300
QY 3301 GCTTGTACGAGCTCAGCGCCGAGACCTCAGTTAGTTGGGCGTTACCTTAACACA 3360
Db 3301 GCTTGTACGAGCTCAGCGCCGAGACCTCAGTTAGTTGGGCGTTACCTTAACACA 3360
QY 3361 CCAAGGTTGCCGCTGTGCGAGGACATGTGAGTTTGTGGAGAGCGTCTTTACAGGCTTC 3420
Db 3361 CCAAGGTTGCCGCTGTGCGAGGACATGTGAGTTTGTGGAGAGCGTCTTTACAGGCTTC 3420
QY 3421 ACCACATGAGAGCCCATTTCTTGTCCAGACTAAGCAGGAGAGAGCACTTCCCTAC 3480
Db 3421 ACCACATGAGAGCCCATTTCTTGTCCAGACTAAGCAGGAGAGAGCACTTCCCTAC 3480
QY 3481 CTGTGTAGCATACCAAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCCTGTGGAG 3540
Db 3481 CTGTGTAGCATACCAAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCCTGTGGAG 3540
QY 3541 CAAATGTGAAGTGTCTCTAAGGCTTAAGGCTTACGTCGACAGGCGCAAGCCCTCTCTG 3600
Db 3541 CAAATGTGAAGTGTCTCTAAGGCTTAAGGCTTACGTCGACAGGCGCAAGCCCTCTCTG 3600
QY 3601 TATAGGCTGGAGCGGTTCAAAACAGAGTTACTACACACACCCCATTAACCAATATATC 3660
Db 3601 TATAGGCTGGAGCGGTTCAAAACAGAGTTACTACACACACCCCATTAACCAATATATC 3660
QY 3661 ATGGCATGATGTCGGCTGACCTGAGAGTGTGTCACAGACACTGGGTGTGTGGGGA 3720
Db 3661 ATGGCATGATGTCGGCTGACCTGAGAGTGTGTCACAGACACTGGGTGTGTGGGGA 3720
QY 3721 GTCTAGCAGCTCTGCGCCGCTATTGCTGTGACAAACAGGCGAGGCTGATTTGTGGAGG 3780
Db 3721 GTCTAGCAGCTCTGCGCCGCTATTGCTGTGACAAACAGGCGAGGCTGATTTGTGGAGG 3780
QY 3781 ATATCTTGTGTCGGGAAGCGCGGCATCATTCGCCAGAGGGAAGTCTTTACCGGAGTTC 3840
Db 3781 ATATCTTGTGTCGGGAAGCGCGGCATCATTCGCCAGAGGGAAGTCTTTACCGGAGTTC 3840
QY 3841 GATGAGATGGAAGTGTGCGCTCACACCTCCCTTACATCAAGAAAGGAAATCACTGCGC 3900
Db 3841 GATGAGATGGAAGTGTGCGCTCACACCTCCCTTACATCAAGAAAGGAAATCACTGCGC 3900
QY 3901 GAACATTTAAACAGAGGCAATGGGTTGCTGCAAAACAGCCACCAACCAAGCGGAGGCT 3960
Db 3901 GAACATTTAAACAGAGGCAATGGGTTGCTGCAAAACAGCCACCAACCAAGCGGAGGCT 3960
QY 3961 GCTGCTCCGCTGGTGAATCCAAAGTGGCGGAGCCCTCGAAGCTTCTGGGCAACATATG 4020
Db 3961 GCTGCTCCGCTGGTGAATCCAAAGTGGCGGAGCCCTCGAAGCTTCTGGGCAACATATG 4020
QY 4021 TGGAAATTCATCAGCGGATACAAATATTTAGCAGGCTTGTCACTCTGCGCAACCC 4080
Db 4021 TGGAAATTCATCAGCGGATACAAATATTTAGCAGGCTTGTCACTCTGCGCAACCC 4080
QY 4081 GCGATGACATGATGTCATTTCAAGGCTTATCACCAGCGGCTCACCACCCACAT 4140
Db 4081 GCGATGACATGATGTCATTTCAAGGCTTATCACCAGCGGCTCACCACCCACAT 4140
QY 4141 ACCCTCTGTTTAACTCTGGGGGAGTGGGTGGCGCCCAACTGTCTCTCCAGGCT 4200
Db 4141 ACCCTCTGTTTAACTCTGGGGGAGTGGGTGGCGCCCAACTGTCTCTCCAGGCT 4200

QY 4201 GCTTCTGCTTGTAGAGCGCGGATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG 4260
Db 4201 GCTTCTGCTTGTAGAGCGCGGATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG 4260
QY 4261 AAGTGTCTTGTGATATTTTGGCAGGTTATGGACAGGAGGTGGCAGCGGCTGTGGCC 4320
Db 4261 AAGTGTCTTGTGATATTTTGGCAGGTTATGGACAGGAGGTGGCAGCGGCTGTGGCC 4320
QY 4321 TTTAAGTCATGAGCGGAGATGCCCTCCACCGAGAACTGGTAACTACTCCCTGCT 4380
Db 4321 TTTAAGTCATGAGCGGAGATGCCCTCCACCGAGAACTGGTAACTACTCCCTGCT 4380
QY 4381 ATCTCTCCCTGGGCGCCTAGTGTGCGGGGTCTGTGCGCAGGATACTGTGCGCAC 4440
Db 4381 ATCTCTCCCTGGGCGCCTAGTGTGCGGGGTCTGTGCGCAGGATACTGTGCGCAC 4440
QY 4441 GTGGGCCAGGAGGAGGAGGCTGTGAGTGAATGAACCGGCTGATAGCGTTCGTCGG 4500
Db 4441 GTGGGCCAGGAGGAGGAGGCTGTGAGTGAATGAACCGGCTGATAGCGTTCGTCGG 4500
QY 4501 GGTAAACAGGTCCTCCCGACACTATGTGCTGAGAGCGAGCTGCGACAGTGTACT 4560
Db 4501 GGTAAACAGGTCCTCCCGACACTATGTGCTGAGAGCGAGCTGCGACAGTGTACT 4560
QY 4561 CAGATCTCTCTAGTCTTACCATCAGTACGTGCTGAAGAGGCTTCACCACTGATCAC 4620
Db 4561 CAGATCTCTCTAGTCTTACCATCAGTACGTGCTGAAGAGGCTTCACCACTGATCAC 4620
QY 4621 GAGGAGTGTGTCAGCGCATGCTCGGCTGTGAGTGAAGAGTGTGGATTTGGATATGC 4680
Db 4621 GAGGAGTGTGTCAGCGCATGCTCGGCTGTGAGTGAAGAGTGTGGATTTGGATATGC 4680
QY 4681 ACGGTGTGATGATTTTCAAGACGTGCTCCAGTCCAGTCTGTCCGCGATTTGCGGGA 4740
Db 4681 ACGGTGTGATGATTTTCAAGACGTGCTCCAGTCCAGTCTGTCCGCGATTTGCGGGA 4740
QY 4741 GTCCCTCTTCTCATGTCACAGTGGGTACAAAGGAGTGTGGGGGCGAGCGCATATG 4800
Db 4741 GTCCCTCTTCTCATGTCACAGTGGGTACAAAGGAGTGTGGGGGCGAGCGCATATG 4800
QY 4801 CAACACCTTGCCATGTGAGACACGATCACCGGACATGTGAAGAAAGGTTCCATGAGG 4860
Db 4801 CAACACCTTGCCATGTGAGACACGATCACCGGACATGTGAAGAAAGGTTCCATGAGG 4860
QY 4861 ATGCTGGGCGCTAGGACCTGTATACACGTGGGATGGAATATCCCATTAAGCGCTAC 4920
Db 4861 ATGCTGGGCGCTAGGACCTGTATACACGTGGGATGGAATATCCCATTAAGCGCTAC 4920
QY 4921 ACCAGGCGCCCTGACGCGCTCCCGGCGCAATTAATTTAGGGCGCTGTGGCGGCTG 4980
Db 4921 ACCAGGCGCCCTGACGCGCTCCCGGCGCAATTAATTTAGGGCGCTGTGGCGGCTG 4980
QY 4981 GCTGCTGAGAGTATAGTGAAGTTACGGGAGTGGGGATTTCCTACGTACGAGGAGATG 5040
Db 4981 GCTGCTGAGAGTATAGTGAAGTTACGGGAGTGGGGATTTCCTACGTACGAGGAGATG 5040
QY 5041 ACCACTGACACAGTAAAGTGGCGGTGTGAGGTTCCGCGCCCGCAATTTCTTACAGAAAGT 5100
Db 5041 ACCACTGACACAGTAAAGTGGCGGTGTGAGGTTCCGCGCCCGCAATTTCTTACAGAAAGT 5100
QY 5101 GATGGGTCGCTTGCACAGATACCTCTCAGCGTGCACAAACCCCTCTCAGGAGAGGTC 5160
Db 5101 GATGGGTCGCTTGCACAGATACCTCTCAGCGTGCACAAACCCCTCTCAGGAGAGGTC 5160
QY 5161 ACATTCCTGTCGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATGGAGCCGAA 5220
Db 5161 ACATTCCTGTCGGGCTCAATCAATACCTGTTGGGTACAGCTCCCATGGAGCCGAA 5220
QY 5221 CCGGACGTAGCATGCTCATTTCTCATGCTCACCGACCCCTTCCCATTTAGGGGAGACG 5280
Db 5221 CCGGACGTAGCATGCTCATTTCTCATGCTCACCGACCCCTTCCCATTTAGGGGAGACG 5280

QY	5281	GCTAAGGCTGAGGCGGAGGAGATCTCCCGCTTGGCCAGGCTATAGCTATGACGAG	5340
Db	5281	GCTAAGGCTAAGCTGAGGCGGAGGAGATCTCCCGCTTGGCCAGGCTATAGCTATGACGAG	5340
QY	5341	CTGTCTCGGCTTCTTGAAGGCAACATGCACATACCGGTATGACTCTCCCGAGCGCTGAC	5400
Db	5341	CTGTCTCGGCTTCTTGAAGGCAACATGCACATACCGGTATGACTCTCCCGAGCGCTGAC	5400
QY	5401	CTCATCGAGGCAACCTCCGTGGCGGAGAGATGGGGGGAACATACCCGCGTGGAG	5460
Db	5401	CTCATCGAGGCAACCTCCGTGGCGGAGAGATGGGGGGAACATACCCGCGTGGAG	5460
QY	5461	TCAGAAAATAAGAGTATATTTTGGACTCTTTCGAGCCGCTCCAGCGGAGAGATGAG	5520
Db	5461	TCAGAAAATAAGAGTATATTTTGGACTCTTTCGAGCCGCTCCAGCGGAGAGATGAG	5520
QY	5521	AGGGAAGATCCGTTCCGGGGAGAGATCCTGGAGGTCGAGAAATTCCTCGAGGAG	5580
Db	5521	AGGGAAGATCCTGTTCCGGGGAGAGATCCTGGAGGTCGAGAAATTCCTCGAGGAG	5580
QY	5581	CCCATATGGGCAACGCCGATTTACAAACCTTCACACTGTTAAGTCTTGAAGAGACCCGAC	5640
Db	5581	CCCATATGGGCAACGCCGATTTACAAACCTTCACACTGTTAAGTCTTGAAGAGACCCGAC	5640
QY	5641	TACGTCCCTCCAGTGTACACAGGGGTTCACATTCGCGCTCCGAAAGGCCCTCCGATACCA	5700
Db	5641	TACGTCCCTCCAGTGTACACAGGGGTTCACATTCGCGCTCCGAAAGGCCCTCCGATACCA	5700
QY	5701	CCTCCAGGAGAGAGAGAGAGGTTGTCTCTGACAAATCTACCGTGTCTTGTGCTTGGCG	5760
Db	5701	CCTCCAGGAGAGAGAGAGGTTGTCTCTGACAAATCTACCGTGTCTTGTGCTTGGCG	5760
QY	5761	GAGCTCGCACAAAGACCTTCGAGAGCTCGAAATCTGCGGCGCGACAGCGGACAGGCA	5820
Db	5761	GAGCTCGCACAAAGACCTTCGAGAGCTCGAAATCTGCGGCGCGACAGCGGACAGGCA	5820
QY	5821	ACGGCTCTCTCTGACACAGCCCTCCGAGAGAGGCGACCGGGATTCGCAAGCTTGAAGTGTAC	5880
Db	5821	ACGGCTCTCTCTGACACAGCCCTCCGAGAGAGGCGACCGGGATTCGCAAGCTTGAAGTGTAC	5880
QY	5881	TCTTCACATGCCCCCTTGAAGGAGGAGCCGGGGATCCCGATCTCACGAGAGGAGTCTTGG	5940
Db	5881	TCTTCACATGCCCCCTTGAAGGAGGAGCCGGGGATCCCGATCTCACGAGAGGAGTCTTGG	5940
QY	5941	TCTACCGTAACCGAGAGAGGCTAGTAGAGAGCTGCTGTGCTGCTGAGATGCTTACACATGG	6000
Db	5941	TCTACCGTAACCGAGAGAGGCTAGTAGAGAGCTGCTGTGCTGCTGAGATGCTTACACATGG	6000
QY	6001	ACAGAGCGCCCTGATACAGCCATGCGCTGCGGAGAGAAACCAAGCTGCCATCAATGCACTG	6060
Db	6001	ACAGAGCGCCCTGATACAGCCATGCGCTGCGGAGAGAAACCAAGCTGCCATCAATGCACTG	6060
QY	6061	AGCAACTCTTTGCTGCGACACCAACTGTGTATGCTTAAATATTCGCAAGGCAAGC	6120
Db	6061	AGCAACTCTTTGCTGCGACACCAACTGTGTATGCTTAAATATTCGCAAGGCAAGC	6120
QY	6121	CTGGGCGAGAGAAAGTACCTTTAGACAGACTGCGAGGTCTCTGACGACCACTACCGGAC	6180
Db	6121	CTGGGCGAGAGAAAGTACCTTTAGACAGACTGCGAGGTCTCTGACGACCACTACCGGAC	6180
QY	6181	GTCGTCAGAGAGATGAGAGGCGCAAGGCGTCCACTTAAGGCTAACTTATCCGTGGAG	6240
Db	6181	GTCGTCAGAGAGATGAGAGGCGCAAGGCGTCCACTTAAGGCTAACTTATCCGTGGAG	6240
QY	6241	GAAGCCTTGAAGCTGACGCCGCCACATTCGGCGAGATCTAAATTTGGCTATGGGCAAG	6300
Db	6241	GAAGCCTTGAAGCTGACGCCGCCACATTCGGCGAGATCTAAATTTGGCTATGGGCAAG	6300
QY	6301	GACGTCGGAACCTATCCAGCAAGGCGGTAAACCAATCCGCTCGGTGGAAAGAGATTTG	6360
Db	6301	GACGTCGGAACCTATCCAGCAAGGCGGTAAACCAATCCGCTCGGTGGAAAGAGATTTG	6360
QY	6361	CTGGAAGCACTGAGACCACTATTTGACCCACCATCATATGGCAAAAAATGAGGTTTTCTGC	6420
Db	6361	CTGGAAGCACTGAGACCACTATTTGACCCACCATCATATGGCAAAAAATGAGGTTTTCTGC	6420
QY	6421	GTCCAAACAGAGAGAGGGGGCCGACGCCAGCTGCTTATGCTATTCACAGATTTGGGG	6480
Db	6421	GTCCAAACAGAGAGAGGGGGCCGACGCCAGCTGCTTATGCTATTCACAGATTTGGGG	6480
QY	6481	GTTCTGTGTGCGAAGAAATGAGCCCTTACATGAGTGGTCTCACCTCCCTCAGAGCGTG	6540
Db	6481	GTTCTGTGTGCGAAGAAATGAGCCCTTACATGAGTGGTCTCACCTCCCTCAGAGCGTG	6540
QY	6541	ATGGGCTCTTATACGAGTTCATATCTCTCTGACACGCGGTCGAGATTCCTGGTAAAT	6600
Db	6541	ATGGGCTCTTATACGAGTTCATATCTCTCTGACACGCGGTCGAGATTCCTGGTAAAT	6600
QY	6601	GCGTGGAAAGCGAAGAAATGCCCTATGGGCTTCGATATGACACCGGCTTTTATGCTCA	6660
Db	6601	GCGTGGAAAGCGAAGAAATGCCCTATGGGCTTCGATATGACACCGGCTTTTATGCTCA	6660
QY	6661	ACGGTCACTGAGATATGACATCCGTTTGAAGAGTAAATCTACCAATGTTGTGACTTGGCC	6720
Db	6661	ACGGTCACTGAGATATGACATCCGTTTGAAGAGTAAATCTACCAATGTTGTGACTTGGCC	6720
QY	6721	CCGGAAGCGACAGAGGACATAGGTGCGTCAAGAGCGGCTTTCATGAGGGGGCCCCGTG	6780
Db	6721	CCGGAAGCGACAGAGGACATAGGTGCGTCAAGAGCGGCTTTCATGAGGGGGCCCCGTG	6780
QY	6781	ACTAATTTCTAAGGGGCGACAACTGGGGCTATGCGCGGTCCGCGAGCGGTCTACTGACG	6840
Db	6781	ACTAATTTCTAAGGGGCGACAACTGGGGCTATGCGCGGTCCGCGAGCGGTCTACTGACG	6840
QY	6841	ACCAGCTGGGTAATACCTCCACATGTTACTTGAAGGGCGCTGCGGCTGTGCAAGCTCG	6900
Db	6841	ACCAGCTGGGTAATACCTCCACATGTTACTTGAAGGGCGCTGCGGCTGTGCAAGCTCG	6900
QY	6901	AAGCTCCAGAGCTGCAAGATGCTGATATGGGAGAGACGACTTGTGTTATCTGTGAAGC	6960
Db	6901	AAGCTCCAGAGCTGCAAGATGCTGATATGGGAGAGACGACTTGTGTTATCTGTGAAGC	6960
QY	6961	GGGGGACCCCAAGAGAGAGGCGAGGACCTACGCGCTTACAGGAGCTATAGTATATAC	7020
Db	6961	GGGGGACCCCAAGAGAGAGGCGAGGACCTACGCGCTTACAGGAGCTATAGTATATAC	7020
QY	7021	TCTGGCCCCCTGGGAGACCGCGCAACACAGAAATCGACTTGGATTTAATACATCATCG	7080
Db	7021	TCTGGCCCCCTGGGAGACCGCGCAACACAGAAATCGACTTGGATTTAATACATCATCG	7080
QY	7081	TCTCCAAATGTGTCAATGCGGACAGATGATCGCAAAAGGGTGTACTATCTCACCCGT	7140
Db	7081	TCTCCAAATGTGTCAATGCGGACAGATGATCGCAAAAGGGTGTACTATCTCACCCGT	7140
QY	7141	GACCCCAACACCCCTTGTGGGGGCTGCTGGAGACAGCTAGACACATCTCAATCAT	7200
Db	71		

Db 7441 TCATGCTCAGGAACCTTG6GGGTACCGCCCTTGGCAGTCTGAGACATCGGGCCAGAGT 7500
QY 7501 GTCCGGCTAGGCTACTGTGCCAGGGGGGAGGGCTGCCACTTGTGGCAGTACTCTTTC 7560
Db 7501 GTCCGGCTAGGCTACTGTGCCAGGGGGGAGGGCTGCCACTTGTGGCAGTACTCTTTC 7560
QY 7561 AACTGGGAGTAGGAGCAGCAAGTCAACTCACTCCAAATCCCGGCTGGCTCCAGATTGGAT 7620
Db 7561 AACTGGGAGTAGGAGCAGCAAGTCAACTCACTCCAAATCCCGGCTGGCTCCAGATTGGAT 7620
QY 7621 TTAATCAGCTGTTGCTGCTGTACAGCGGGGAGACATATATCAGAGCTGTCTCGT 7680
Db 7621 TTAATCAGCTGTTGCTGCTGTACAGCGGGGAGACATATATCAGAGCTGTCTCGT 7680
QY 7681 GCCCGACCCCGGTGTTGATGTGTGCTACTCTTCTGTGTAGGGGTAGGATCTAT 7740
Db 7681 GCCCGACCCCGGTGTTGATGTGTGCTACTCTTCTGTGTAGGGGTAGGATCTAT 7740
QY 7741 CTACTGCCACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTTTT 7800
Db 7741 CTACTGCCACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTTTT 7800
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
QY 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
QY 7921 TTAGCTGTAAGTCCGCTGAGCGGCTGACTGAGAGAGTGTACTGTGCTCTCTG 7980
Db 7921 TTAGCTGTAAGTCCGCTGAGCGGCTGACTGAGAGAGTGTACTGTGCTCTCTG 7980
QY 7981 AGATCAAGT 7989
Db 7981 AGATCAAGT 7989
RESULT 5
AL47277
ID AL47277 standard; DNA; 7992 BP.
AC AAL47277;
XX
XX AAL47277;
XX
XX 30-AUG-2002 (first entry)
XX
XX Hepatitis C virus sub-genomic replicon recombinant clone HCVR2.
DE Hepatitis C virus sub-genomic replicon recombinant clone HCVR2.
XX
XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
KW virulence; hepatotropic; gene therapy; anti-viral; gene; ds.
XX
XX Hepatitis C virus.
OS
XX
XX MO200238793-A2.
XX
XX 16-MAY-2002.
XX
XX 02-NOV-2001; 2001MO-US46350.
XX
XX 07-NOV-2000; 2000US-245866P.
XX
XX (ANAD-) ANADYS PHARM INC.
XX
XX Bichko V;
XX
XX WPI; 2002-490082/52.
XX
XX
XX Novel nucleic acid encoding replication competent recombinant hepatitis
PT C virus genome useful for screening anti-hepatitis C virus therapeutics
and for vaccine development
XX
XX
XX Claim 7; Page 52-56; 85bp; English.

XX
CC The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication complement
CC non-infectious, replication defective infection therapy, and
CC replication-defective non-infectious HCV, in gene therapy or gene
CC vaccination targeted to hepatic tissue for treating an animal infected or
CC susceptible to HCV infection and for studying HCV infection and
CC propagation. The present sequence is a clone of a fragment of the HCV
CC genome designated HCVR2.
XX
SQ Sequence 7992 BP; 1648 A; 2368 C; 2243 G; 1733 T; 0 other:
Query Match 99.9%; Score 7980.8; DB 24; Length 7992;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GCGAGCCCCCGATGGGGGCGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60
Db 1 GCGAGCCCCCGATGGGGGCGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60
QY 61 TCTTACGAGAAAGCGTCAACCATGAGCTTATGATGAGTGTGTGACCTCCAGAC 120
Db 61 TCTTACGAGAAAGCGTCAACCATGAGCTTATGATGAGTGTGTGACCTCCAGAC 120
QY 121 CCCCCCTCCGGGAGAGCATAGTGTGTGAGAACCGGTGAGTACCGGAAATTTGGCA 180
Db 121 CCCCCCTCCGGGAGAGCATAGTGTGTGAGAACCGGTGAGTACCGGAAATTTGGCA 180
QY 181 GAGAGCGGGGTCCTTTTGTGATCAACCCGCTCAATCGATTTGGGCTGCCGCC 240
Db 181 GAGAGCGGGGTCCTTTTGTGATCAACCCGCTCAATCGATTTGGGCTGCCGCC 240
QY 241 GCGAGACTGCTAGCCGATAGTGTGTGAGAACCGGTGAGTACCGGAAATTTGGCA 300
Db 241 GCGAGACTGCTAGCCGATAGTGTGTGAGAACCGGTGAGTACCGGAAATTTGGCA 300
QY 301 GTGCTTGGAGTGGCCCCGAGAGTCTCTAGACCGGTGACCATGAGCAGCAATCTTAAC 360
Db 301 GTGCTTGGAGTGGCCCCGAGAGTCTCTAGACCGGTGACCATGAGCAGCAATCTTAAC 360
QY 361 CTCAAAGAAAACCAAGGGGCGGCATGATTGAACAAGATGATTCAGACGAGTTCTC 420
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QY 421 CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACAACAATGGGCTGCT 480
Db 421 CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACAACAATGGGCTGCT 480
QY 481 CTGATGCGCGCGGTGTCGCGGCTGTCAGCGCAGGGGCGCGGTCTTTTGTCAAGACG 540
Db 481 CTGATGCGCGCGGTGTCGCGGCTGTCAGCGCAGGGGCGCGGTCTTTTGTCAAGACG 540
QY 541 ACCCTGCGGTCCTCTGATGATGACTGAGAGAGGAGGAGCGGCTATCTGTGGCTGCGCA 600
Db 541 ACCCTGCGGTCCTCTGATGATGACTGAGAGAGGAGGAGCGGCTATCTGTGGCTGCGCA 600
QY 601 CGAGCGGGGCTTCTTGGCCAGCTGTGCTGACAGCTTTGCTGAAGCGGAGAGGACTGGC 660
Db 601 CGAGCGGGGCTTCTTGGCCAGCTGTGCTGACAGCTTTGCTGAAGCGGAGAGGACTGGC 660
QY 661 TCGTATTGGGCGAAGTGCAGGGGAGATCTCCCTGTCATCTCACTGCTCTGCGGAGA 720
Db 661 TCGTATTGGGCGAAGTGCAGGGGAGATCTCCCTGTCATCTCACTGCTCTGCGGAGA 720
QY 721 AAGTATCATATGAGCTGATGCAATGGGCGGCTGATAGCGCTTGATCCGAGTCTGCC 780
Db 721 AAGTATCATATGAGCTGATGCAATGGGCGGCTGATAGCGCTTGATCCGAGTCTGCC 780

Db 2941 AAGCTGTCCGGCTCGGACTCATGTCTAGCATATTAACGGGCGCTTGATGTAATCCGTC 3000
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Db 3121 CTGAGCCGACCTTACCATTTAGAGAGAGCGGTGACAGAGAGCGGTGTACGCTG 3180
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Qy 7561 AACTGGGCACTAAGACCAAGCTCAAACTCACTCCAAATCCGGCTGCCAGTTGGAT 7620
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Qy 7981 AGATCAGTACT 7992
Db 7981 AGATCAGTACT 7992

RESULT 6
ID AAL47280 standard; DNA; 7992 BP.
XX AAL47280;
XX AC
XX 30-AUG-2002 (first entry)
XX DE Hepatitis C virus sub-genomic replicon recombinant clone HCVR22.
XX XX
XX KM Hepatitis: HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
XX KM viraemia; hepatocellular; gene therapy; anti-viral; gene; ds.
XX OS Hepatitis C virus.
XX PN WO200238793-A2.
XX PD 16-MAY-2002.
XX PF 02-NOV-2001; 2001WO-US46350.
XX PR 07-NOV-2000; 2000US-245866P.
XX PA (ANAD-) ANADYS PHARM INC.
XX XX
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PI Bichko V;
XX WPI: 2002-490082/52.
DR
XX
XX PT Novel nucleic acid encoding replication competent recombinant hepatitis
XX C virus genome useful for screening anti-hepatitis C virus therapeutics
XX and for vaccine development -
XX
XX Claim 10; Page 66-70; 85pp; English.
XX
XX The present invention provides protein and coding sequences from
XX Hepatitis C virus (HCV), comprising all or part of the HCV genome and
XX able to replicate efficiently when transfected into a susceptible cell
XX line without reducing the growth rate of the cell line by more than 10
XX fold. The sequences are useful for screening for anti-HCV therapeutics,
XX for detecting antibodies to HCV in a biological sample such as blood,
XX serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
XX for deriving authentic HCV components such as replication-complement
XX CC non-infectious, replication-defective infection-component, and
XX CC replication-targeted non-infectious HCV, in gene therapy or gene
XX CC vaccination targeted to hepatic tissue for treating an animal infected or
XX CC susceptible to HCV infection and for studying HCV infection and
XX CC propagation. The present sequence is a clone of a fragment of the HCV
XX genome designated HCVR22.
XX
XX Sequence 7992 BP; 1646 A; 2368 C; 2245 G; 1733 T; 0 other:
SQ
Query Match 99.9%; Score 7980.8; DB 24; Length 7992;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7985; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GCCAGCCCCGATTTGGGGGCGACCTCCACCTATGATCACTCCCTGTGAGGACTACTG 60
Db 1 GCCAGCCCCGATTTGGGGGCGACCTCCACCTATGATCACTCCCTGTGAGGACTACTG 60
Qy 61 TCTTCACGAGAAAGGCTGTAGCCATGAGGCTAGTATGATGATGATGATGATGATGATG 120
Db 61 TCTTCACGAGAAAGGCTGTAGCCATGAGGCTAGTATGATGATGATGATGATGATGATG 120
Qy 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTAGTACACCGGAATTTGCCAG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTAGTACACCGGAATTTGCCAG 180
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Db 181 GACGACCGGGTCTCTTCTTGTATCAACCGCTCAATGCTGTGAGATTTGGGGTCCGCC 240
Qy 241 GCGAGACTGCTAGCCGAGTAGTGTGTTGGCGGAAGGCTTTGTGTACTGCTGATAGG 300
Db 241 GCGAGACTGCTAGCCGAGTAGTGTGTTGGCGGAAGGCTTTGTGTACTGCTGATAGG 300
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Db 601 CGAGGGCGTTCTTGGCGAGCTGTGCTGACGTTGTCACTGAAGCGGAGAGGACTGGC 660
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D	b	661	TGCTATTGGGCGAAGTGGCGGGGCGAGATCTCCTGTCACTCTCTCTCTCTCTCTCCGAGA	720
Q	y	721	AAGTATCCATCATGAGTGTGATGCAATGCGGCGGCTGCATACGCTTGATCTGAGTACCTTGC	780
D	b	721	AAGTATCCATCATGAGTGTGATGCAATGCGGCGGCTGCATACGCTTGATCTGAGTACCTTGC	780
Q	y	781	CATTGCGACCCACCAAGGAAATCGATGATGAGCGAGCAAGTACTGGATGGAAGCGGATC	840
D	b	781	CATTGCGACCCACCAAGGAAATCGATGATGAGCGAGCAAGTACTGGATGGAAGCGGATC	840
Q	y	841	TTTGATGATCAGATGATCTGGAGCAAGAGCATCAGGGGCTGGCGCCAGACCGCACTGTTGC	900
D	b	841	TTTGATGATCAGATGATCTGGAGCAAGAGCATCAGGGGCTGGCGCCAGACCGCACTGTTGC	900
Q	y	901	CCAGGCTCAAGGGGCGGATCCCCGAGCGGAGAGTCTGCTGTGACCCATGAGCATGGCT	960
D	b	901	CCAGGCTCAAGGGGCGGATCCCCGAGCGGAGAGTCTGCTGTGACCCATGAGCATGGCT	960
Q	y	961	GCTTTCGCAATATCATGTTGAGAAATGCGCCCTTTTCTGATATCATCATGTTGGCGGC	1020
D	b	961	GCTTTCGCAATATCATGTTGAGAAATGCGCCCTTTTCTGATATCATCATGTTGGCGGC	1020
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D	b	1021	TGGTGTGGGGGAGCCGCTATCAGACATATGCGTGGCTACCCGTAATATGCTGAGAGC	1080
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D	b	1141	AGGCAATCGCCTTCTATCGCCTCTTGAGAGTCTTCTGATATTAATTAACAGACCAACG	1200
Q	y	1201	GTTTCCCTCTAGGCGGATCATTTCCGCCCTCTCCCTCCCCCCCCCTAAGCTTACTGCG	1260
D	b	1201	GTTTCCCTCTAGGCGGATCATTTCCGCCCTCTCCCTCCCCCCCCCTAAGCTTACTGCG	1260
Q	y	1261	CGAAGCGCTGTGAATAGCCCGGCTGTGCTTGTATATGTATTTTCCACCATATG	1320
D	b	1261	CGAAGCGCTGTGAATAGCCCGGCTGTGCTTGTATATGTATTTTCCACCATATG	1320
Q	y	1321	CCGTTCTTTGGCAATGTGAGGCGCCCGGAAACCTGGCCCTGTCTTCTTGACAGCATTCCT	1380
D	b	1321	CCGTTCTTTGGCAATGTGAGGCGCCCGGAAACCTGGCCCTGTCTTCTTGACAGCATTCCT	1380
Q	y	1381	AGGGGTCTTCCCTCTCGCCAAAGAGATCAAGTCTGTGATATGTCGTGAAGAGCA	1440
D	b	1381	AGGGGTCTTCCCTCTCGCCAAAGAGATCAAGTCTGTGATATGTCGTGAAGAGCA	1440
Q	y	1441	GTTCTCTGGAAGCTTCTTGAAGCAACAACCTCTGTAGCAACCTTTTGACGGGAGGG	1500
D	b	1441	GTTCTCTGGAAGCTTCTTGAAGCAACAACCTCTGTAGCAACCTTTTGACGGGAGGG	1500
Q	y	1501	AACCCCGCACTGTGCGAGAGTGGCTGTGGGCGAAAGCCAGCTGATATACATACACT	1560
D	b	1501	AACCCCGCACTGTGCGAGAGTGGCTGTGGGCGAAAGCCAGCTGATATACATACACT	1560
Q	y	1561	GCAAGGCGGCAACAACCCAGTGGCAAGTGTGATGATGTTGTAAGAGATCAAA	1620
D	b	1561	GCAAGGCGGCAACAACCCAGTGGCAAGTGTGATGATGTTGTAAGAGATCAAA	1620
Q	y	1621	TGGCTCTCTCAAGGATATCAACAAGGGCTAAAGATATGCCAGAGGTACCCATGTT	1680
D	b	1621	TGGCTCTCTCAAGGATATCAACAAGGGCTAAAGATATGCCAGAGGTACCCATGTT	1680
Q	y	1681	ATGGGATCTGATCTGGGGGCTCGGTGTGACATGTTTACATGTTTGAAGCGAGTTAAA	1740
D	b	1681	ATGGGATCTGATCTGGGGGCTCGGTGTGACATGTTTACATGTTTGAAGCGAGTTAAA	1740

QY	1741	AACTATGAGCCCCCGAAGACAGCGGAGAGTGGTTTCTCTTGGAAAAACAGATAATACC	1800
Db	1741	AACTGTAGGCCCCCGGAATACAGCGGAGAGTGGTTTCTCTTGGAAAAACAGATAATACC	1800
QY	1801	ATGCGCCCTATTAGGGCTACTCTCCACAGACGCGAGGCTTACTTGGCTGATCATACT	1860
Db	1801	ATGCGCGCCTATTAGGGCTACTCTCCACAGACGCGAGGCTTACTTGGCTGATCATACT	1860
QY	1861	AGCCTCAGAGCCGGGACAGAGAACCGAGTGCAGGGGAGAGTCCACAGTGGTCTCCACGGCA	1920
Db	1861	AGCCTCAGAGCCGGGAGACAGAGAACCGAGTGCAGGGGAGAGTCCAAAGTGGTCTCCACGGCA	1920
QY	1921	ACACATCTTTCCTGGCGACCTGCGTCAATGGCGTGTGTGGACTGTCTATCATGTGTGC	1980
Db	1921	ACACAACTTTCCTGGGAGACTCTCGTCAATGGCGTGTGTGGACGTCTATCATGTGTGC	1980
QY	1981	GGCTCAAGAGCCCTTGGCGGCCCCCAAGGGGCCCAATCACCAATATGACCAATGTGGAC	2040
Db	1981	GGCTCAAGAGCCCTTGGCGGCCCCCAAGGGGCCCAATCACCAATATGACCAATGTGGAC	2040
QY	2041	CAGAGCCTCGTGGCTGGCAAGCGCCCCCGGGGGCGCTTCTTGACACCATGCACTGCG	2100
Db	2041	CAGAGCCTCGTGGCTGGCAAGCGCCCCCGGGGGCGCTTCTTGACACCATGCACTGCG	2100
QY	2101	GGCAGCTCGAGACCTTTACTTGGTCAAGAGACATGGCGATGTATTGCGGTGCGCGGGGG	2160
Db	2101	GGCAGCTCGAGACCTTTACTTGGTCAAGAGACATGGCGATGTATTGCGGTGCGCGGGGG	2160
QY	2161	GGCGACAGCAGGGGAGACCTACTCTGCCACAGGCCCGTCTCCTACTTGAAGGGCTCTTGG	2220
Db	2161	GGCGACAGCAGGGGAGACCTACTCTGCCACAGGCCCGTCTCCTACTTGAAGGGCTCTTGG	2220
QY	2221	GGCGGTCCACAGTGCCTGCCCCCTGGGGGACAGCTGTGGGCACTTTTGGGGTCCGGTGTGCG	2280
Db	2221	GGCGGTCCACAGTGCCTGCCCCCTGGGGGACAGCTGTGGGCACTTTTGGGGTCCGGTGTGCG	2280
QY	2281	ACCCGAGGGGTTGGGAAGGGCGGTGGACTTTGTACCCCGTGAATCATGGAACCACTATG	2340
Db	2281	ACCCGAGGGGTTGGGAAGGGCGGTGGACTTTGTACCCCGTGAATCATGGAACCACTATG	2340
QY	2341	CGGTGCCCGGTTCAGGAGCAACTGTGCCCTCGGGCGGTACCGCAGCAATCCAGGTG	2400
Db	2341	CGGTGCCCGGTTCAGGAGCAACTGTGCCCTCGGGCGGTACCGCAGCAATCCAGGTG	2400
QY	2401	GCCCATCTACACGGCCCTACTGTGTAGGGGCAAGAGCACTAAGGTGCCGGCTGTGATGCA	2460
Db	2401	GCCCATCTACACGGCCCTACTGTGTAGGGGCAAGAGCACTAAGGTGCCGGCTGTGATGCA	2460
QY	2461	GCCCAAGGGTAAAGGTGTGTGTCTGTCTGAACCCGTCCGTGGCGCCACCTAGTGTGGG	2520
Db	2461	GCCCAAGGGTAAAGGTGTGTGTCTGTCTGAACCCGTCCGTGGCGCCACCTAGTGTGGG	2520
QY	2521	GGGTATATGTATAAGGACATGTATGATGACACCTAATCAGAAACGGGGTATGAGACATC	2580
Db	2521	GGGTATATGTATAAGGACATGTATGATGACACCTAATCAGAAACGGGGTATGAGACATC	2580
QY	2581	ACCCAGGGTGGCCCCCATCAGTACTCCACTATGSAAGTTCTTGGCGACGCGTGTGGC	2640
Db	2581	ACCCAGGGTGGCCCCCATCAGTACTCCACTATGSAAGTTCTTGGCGACGCGTGTGGC	2640
QY	2641	TCTGGGGCGGCTATGACATCATATATATGTGATGAGTGGCACTCAACTGACTCGACCACT	2700
Db	2641	TCTGGGGCGGCTATGACATCATATATATGTGATGAGTGGCACTCAACTGACTCGACCACT	2700
QY	2701	ATTCCTGGGCAATCGGCAAGTCTGTGACAAAGCGGAAGCGGTGGAGCGGCACTCGTGGT	2760
Db	2701	ATTCCTGGGCAATCGGCAAGTCTGTGACAAAGCGGAAGCGGTGGAGCGGCACTCGTGGT	2760
QY	2761	CTCGGCACCGCTTAGCGCTTCGGAGATCGTACCGGTCCACATCCAAACATTCAGGAGGTTG	2820
Db	2761	CTCGGCACCGCTTAGCGCTTCGGAGATCGTACCGGTCCACATCCAAACATTCAGGAGGTTG	2820

QY 2821 GCTGTGTCAGACACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACATC 2880
DB 2821 GCTGTGTCAGACACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACATC 2880
QY 2881 AAGGGGGGAGGACACTCTATTTCGCAATCCAGAGAAATGATGATGACCTGGCGG 2940
DB 2881 AAGGGGGGAGGACACTCTATTTCGCAATCCAGAGAAATGATGATGACCTGGCGG 2940
QY 2941 AAGCTGTCCGGCTGGGACTCAATGCTGTAGCATATTAACCGGGGCTTGATGTATCC 3000
DB 2941 AAGCTGTCCGGCTGGGACTCAATGCTGTAGCATATTAACCGGGGCTTGATGTATCC 3000
QY 3001 ATACCAACTAGGAGAGACATCATGTGCTAGCAAGGAGCGCTTAATGAGCGGTTTACC 3060
DB 3001 ATACCAACTAGGAGAGACATCATGTGCTAGCAAGGAGCGCTTAATGAGCGGTTTACC 3060
QY 3061 GGGGATTTGACTCACTGATGACTGCAATACATGTGTACCCAGACAGTGCAGTTGAGC 3120
DB 3061 GGGGATTTGACTCACTGATGACTGCAATACATGTGTACCCAGACAGTGCAGTTGAGC 3120
QY 3121 CTGGACCCGACCTTCACCATTTGAGAGAGACCGCTGCCAAGAGCGGCTGTACGCTCG 3180
DB 3121 CTGGACCCGACCTTCACCATTTGAGAGAGACCGCTGCCAAGAGCGGCTGTACGCTCG 3180
QY 3181 CACGGCGAGGACGAGACTGTAGGGGAGAGATGGGCATTTACAGGTTTGTACTCCAGGA 3240
DB 3181 CACGGCGAGGACGAGACTGTAGGGGAGAGATGGGCATTTACAGGTTTGTACTCCAGGA 3240
QY 3241 GAACGGCCCTCGGGCATGTTCATTCCTGCTGTGTGCGAGTGTATAGCGGGGCTGT 3300
DB 3241 GAACGGCCCTCGGGCATGTTCATTCCTGCTGTGTGCGAGTGTATAGCGGGGCTGT 3300
QY 3301 GCTGTGAGAGACTACGCGCGCGAGACCTAGTTAGTTGCGGGCTTACTTAACACA 3360
DB 3301 GCTGTGAGAGACTACGCGCGCGAGACCTAGTTAGTTGCGGGCTTACTTAACACA 3360
QY 3361 CCAAGGTTGGCTGTGCGACAGACATCTGAGATTCTGGAGAGCGCTTTTACAGGCTC 3420
DB 3361 CCAAGGTTGGCTGTGCGACAGACATCTGAGATTCTGGAGAGCGCTTTTACAGGCTC 3420
QY 3421 ACCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGAGAGACACTTCCCTAC 3480
DB 3421 ACCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGAGAGACACTTCCCTAC 3480
QY 3481 CTGTAGCATACCAAGCTGAGGCTGTGCGCAGGCTCAGGCTCCACCTCATCTGTGGAC 3540
DB 3481 CTGTAGCATACCAAGCTGAGGCTGTGCGCAGGCTCAGGCTCCACCTCATCTGTGGAC 3540
QY 3541 CAATGTGGAAGTGTCTCATAGGCTAAAGCCAGCTCAGCGGGCAACGCCCTGTG 3600
DB 3541 CAATGTGGAAGTGTCTCATAGGCTAAAGCCAGCTCAGCGGGCAACGCCCTGTG 3600
QY 3601 TATAGCTGGAGACCTTCAAAAGAGGTTACTACACACACCACCAATACAAATACATC 3660
DB 3601 TATAGCTGGAGACCTTCAAAAGAGGTTACTACACACACCACCAATACAAATACATC 3660
QY 3661 ATGGCATGATGTCGGGTGACCTGAGAGTGTGACAGAGACCTGGGTGTGTAGGCGGA 3720
DB 3661 ATGGCATGATGTCGGGTGACCTGAGAGTGTGACAGAGACCTGGGTGTGTAGGCGGA 3720
QY 3721 GTCCTAGCAGCTGTGCGCGGTATTCCTGTACAAAGCAGGAGCGTGTGTTGTGGGCAAG 3780
DB 3721 GTCCTAGCAGCTGTGCGCGGTATTCCTGTACAAAGCAGGAGCGTGTGTTGTGGGCAAG 3780
QY 3781 ATCATCTTGTCCGGAAGCGCGCATTCCTCCGACAGGAAAGTCTTTACCGGGAGTTC 3840
DB 3781 ATCATCTTGTCCGGAAGCGCGCATTCCTCCGACAGGAAAGTCTTTACCGGGAGTTC 3840
QY 3841 GATGAGATGGAAGAGTGGGCTCACAACCTCCCTTACATGGAACAGGAAATGACGTGCGC 3900
DB 3841 GATGAGATGGAAGAGTGGGCTCACAACCTCCCTTACATGGAACAGGAAATGACGTGCGC 3900
QY 3901 GAACAATTCAACAGAAAGCAATCGGCTGTCTCAAAACAGCCACCAAGCAAGCGAGCT 3960

DB 3901 GAACAATTCAACAGAAAGCAATCGGCTGTCTGGAACAGCCACCAAGCAAGCGAGGCT 3960
QY 3961 GCTGTCCCGTGTGGAATCCCAAGTGGCGGACCCCTCGAAGCCTTCTGGGGGAACATATG 4020
DB 3961 GCTGTCCCGTGTGGAATCCCAAGTGGCGGACCCCTCGAAGCCTTCTGGGGGAACATATG 4020
QY 4021 TGGATTTTCATAGCGGGATACAAATTTTACGAGCTGTGTCCATCTGCTGCAACCCC 4080
DB 4021 TGGATTTTCATAGCGGGATACAAATTTTACGAGCTGTGTCCATCTGCTGCAACCCC 4080
QY 4081 GCGATAGCATCACTGATGGCATTCACAGCCTCTATACCAAGCCGCTCACACCAACAT 4140
DB 4081 GCGATAGCATCACTGATGGCATTCACAGCCTCTATACCAAGCCGCTCACACCAACAT 4140
QY 4141 ACCCTCTGTTTAAATCCTGTGGGGGATGGGTGGCCGCCCACTTGTCTCTCCAGCGCT 4200
DB 4141 ACCCTCTGTTTAAATCCTGTGGGGGATGGGTGGCCGCCCACTTGTCTCTCCAGCGCT 4200
QY 4201 GCTTGTGCTTGTAGGCGCGGACATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG 4260
DB 4201 GCTTGTGCTTGTAGGCGCGGACATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG 4260
QY 4261 AAGTGCTTGTGGAATTTTGTGCAAGTTATGAGCAGGAGGTTGCAAGCGCGCTGTGGCC 4320
DB 4261 AAGTGCTTGTGGAATTTTGTGCAAGTTATGAGCAGGAGGTTGCAAGCGCGCTGTGGCC 4320
QY 4321 TTTAAGTGTATAGGGGGGAGATGGCTCCACCGGAGACCTGGGTAACCTACTCCCTGCT 4380
DB 4321 TTTAAGTGTATAGGGGGGAGATGGCTCCACCGGAGACCTGGGTAACCTACTCCCTGCT 4380
QY 4381 ATCCTCTCCCTGTGGCGCCCTAGCTGTGGGCTGTGTGCGCAGCGAATCTGCTGCGAC 4440
DB 4381 ATCCTCTCCCTGTGGCGCCCTAGCTGTGGGCTGTGTGCGCAGCGAATCTGCTGCGAC 4440
QY 4441 GTGGGCCCAAGGGAGGGGCTGTGCAAGTGAACCGGCTGTGAGCTTGTGCTGGGG 4500
DB 4441 GTGGGCCCAAGGGAGGGGCTGTGCAAGTGAACCGGCTGTGAGCTTGTGCTGGGG 4500
QY 4501 GGTAAACAGCTGTCCCGCAGCAGTATGTGCTGAGAGCAGCTGACAGCGGTGAC 4560
DB 4501 GGTAAACAGCTGTCCCGCAGCAGTATGTGCTGAGAGCAGCTGACAGCGGTGAC 4560
QY 4561 CAGATCCTCTAGTCTTACCATCACTGAGCTGCTGAGAGGCTTACACAGTGAATAC 4620
DB 4561 CAGATCCTCTAGTCTTACCATCACTGAGCTGCTGAGAGGCTTACACAGTGAATAC 4620
QY 4621 GAGGACTGTGTCACGCGCATGTCCGCTGTGCTAAGAGATTTTGGGATTTGATATGC 4680
DB 4621 GAGGACTGTGTCACGCGCATGTCCGCTGTGCTAAGAGATTTTGGGATTTGATATGC 4680
QY 4681 ACGGTGTGATGATTTCAAGACCTGCTCCAGCTCAAGCTCTGCGGATGTGCGGGA 4740
DB 4681 ACGGTGTGATGATTTCAAGACCTGCTCCAGCTCAAGCTCTGCGGATGTGCGGGA 4740
QY 4741 GTCCCTCTTCTCATGTCAAGCTGGGTCAAGAGAGTGTGGCGGGCGACGCAATATG 4800
DB 4741 GTCCCTCTTCTCATGTCAAGCTGGGTCAAGAGAGTGTGGCGGGCGACGCAATATG 4800
QY 4801 CAACACACCTGCCATGTGAGAGACAGATCACCAGCAATGTAAAAAGGTTCCATGAGG 4860
DB 4801 CAACACACCTGCCATGTGAGAGACAGATCACCAGCAATGTAAAAAGGTTCCATGAGG 4860
QY 4861 ATGCTGGGGCTAGGACCTGTAGTAACAGTGGCATGAAATTCCTTAACCGCTAC 4920
DB 4861 ATGCTGGGGCTAGGACCTGTAGTAACAGTGGCATGAAATTCCTTAACCGCTAC 4920
QY 4921 ACCAGGGCCCTGTGCAAGCGCTTCCCGGGCCAAATTAATTTAGGGGCTGTGGGJSTG 4980
DB 4921 ACCAGGGCCCTGTGCAAGCGCTTCCCGGGCCAAATTAATTTAGGGGCTGTGGGJSTG 4980
QY 4981 GCTGCTAGGAGTACGTGAGGTTACGGGGGTGGGGATTTCCATAGTACGGGCAATG 5040

Db 4981 GGTGCTGAGAGTAGTGAAGTTACGGGGTGGGGGATTTCACATAGTACAGGGCATG 5040
QY 5041 ACCACTGACAAAGTAAGTCCCGGTGAGGTTCCGGCCCCCGAATTCCTTCACAGAAATG 5100
Db 5042 ACCACTGACAAAGTAAGTCCCGGTGAGGTTCCGGCCCCCGAATTCCTTCACAGAAATG 5100
QY 5101 GATGGGTGCGGTGACAGTAGTACAGTCCAGAGTGCACAAACCCCTCTACGGAGAGATG 5160
Db 5101 GATGGGTGCGGTGACAGTAGTACAGTCCAGAGTGCACAAACCCCTCTACGGAGAGATG 5160
QY 5161 ACATTCCTGCTGCGGTGACAGTACATCAATACCTGTTGGGTGACAGCTCCATGCGAGCCGAA 5220
Db 5161 ACATTCCTGCTGCGGTGACAGTACATCAATACCTGTTGGGTGACAGCTCCATGCGAGCCGAA 5220
QY 5221 CCGAGGTAGAGTGTCTCTCTCCATGCTACAGCCAGCCCTCCCATATACGGAGAGATG 5280
Db 5221 CCGAGGTAGAGTGTCTCTCTCCATGCTACAGCCAGCCCTCCCATATACGGAGAGATG 5280
QY 5281 GCTAAGCCTAGAGTGTGCGAGGGAGTCTCCCTCTCTGCGAGTCAATCAGTACAGTACG 5340
Db 5281 GCTAAGCCTAGAGTGTGCGAGGGAGTCTCCCTCTCTGCGAGTCAATCAGTACAGTACG 5340
QY 5341 CTGTCTGCGGCTTCTCTGAGAGCAATGCACTACCCCTCATGACTCCCGGAGCGTAC 5400
Db 5341 CTGTCTGCGGCTTCTCTGAGAGCAATGCACTACCCCTCATGACTCCCGGAGCGTAC 5400
QY 5401 CTCATGAGAGCAACCTCTCTGAGAGCAATGCACTACCCCTCATGACTCCCGGAGCGTAC 5460
Db 5401 CTCATGAGAGCAACCTCTCTGAGAGCAATGCACTACCCCTCATGACTCCCGGAGCGTAC 5460
QY 5461 TCAGAAATAAGTAATTTTGGACTTTTCGAGCTTTTCGAGCCGCTCAAGCGAGAGAGATG 5520
Db 5461 TCAGAAATAAGTAATTTTGGACTTTTCGAGCTTTTCGAGCCGCTCAAGCGAGAGATG 5520
QY 5521 AAGGAGATATCCGTTCCGGGAGAGATCTCGGAGAGTGCAGAAATTCCTCGAGAGTAC 5580
Db 5521 AAGGAGATATCCGTTCCGGGAGAGATCTCGGAGAGTGCAGAAATTCCTCGAGAGTAC 5580
QY 5581 CCCATATGGGAGAGCCCGGATTAACACCTCTCATCTGTAAGTCTCTGAGAGAGCCGAG 5640
Db 5581 CCCATATGGGAGAGCCCGGATTAACACCTCTCATCTGTAAGTCTCTGAGAGAGCCGAG 5640
QY 5641 TAGTCTCTGAGTGTACAGAGTGTGCTATGCGGCTCGCAAGAGCCCTCCGATACCA 5700
Db 5641 TAGTCTCTGAGTGTACAGAGTGTGCTATGCGGCTCGCAAGAGCCCTCCGATACCA 5700
QY 5701 CCTCAAGAGAGAGAGAGTGTCTCTGAGATCTACCGTGTCTTCTGAGTGTGCG 5760
Db 5701 CCTCAAGAGAGAGAGAGTGTCTCTGAGATCTACCGTGTCTTCTGAGTGTGCG 5760
QY 5761 GAGTGTGAGAGAGAGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGAGAGAGAGAG 5820
Db 5761 GAGTGTGAGAGAGAGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGAGAGAGAGAG 5820
QY 5821 ACAGGCTCTCTGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5880
Db 5821 ACAGGCTCTCTGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5880
QY 5881 TCTTCATGCGCGGCTTGAAGGGAGAGCGGGAGATCCCGATCTCAGAGAGAGAGTGG 5940
Db 5881 TCTTCATGCGCGGCTTGAAGGGAGAGCGGGAGATCCCGATCTCAGAGAGAGAGTGG 5940
QY 5941 TCTACCGTAAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6000
Db 5941 TCTACCGTAAGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6000
QY 6001 ACAGGCGGCTGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6060
Db 6001 ACAGGCGGCTGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6060
QY 6061 AGCAACTCTTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6120
Db 6061 AGCAACTCTTGTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6120

QY 6121 CTGCGGAGAGAGAGAGTCACTTTGACAGACTGCAAGTCTCTGAGAGAGAGAGAGAG 6180
Db 6121 CTGCGGAGAGAGAGAGTCACTTTGACAGACTGCAAGTCTCTGAGAGAGAGAGAGAG 6180
QY 6181 GTGCTCAAGAGATGAG 6240
Db 6181 GTGCTCAAGAGATGAG 6240
QY 6241 GAGGCTGAG 6300
Db 6241 GAGGCTGAG 6300
QY 6301 GAGGCTGAG 6360
Db 6301 GAGGCTGAG 6360
QY 6361 CTGGAAG 6420
Db 6361 CTGGAAG 6420
QY 6421 GTGCAAG 6480
Db 6421 GTGCAAG 6480
QY 6481 GTGCTGAG 6540
Db 6481 GTGCTGAG 6540
QY 6541 ATGAGCTCTTCAATAGAGATCCATATCTCTCTGAGAGAGAGAGAGAGAGAGAG 6600
Db 6541 ATGAGCTCTTCAATAGAGATCCATATCTCTCTGAGAGAGAGAGAGAGAGAGAG 6600
QY 6601 GCTGGAAG 6660
Db 6601 GCTGGAAG 6660
QY 6661 ACAGTCTGAG 6720
Db 6661 ACAGTCTGAG 6720
QY 6721 CCGGAG 6780
Db 6721 CCGGAG 6780
QY 6781 ACTAATTTCAAG 6840
Db 6781 ACTAATTTCAAG 6840
QY 6841 ACCAGTGTGAG 6900
Db 6841 ACCAGTGTGAG 6900
QY 6901 AAGCTCTGAG 6960
Db 6901 AAGCTCTGAG 6960
QY 6961 GCGGGAG 7020
Db 6961 GCGGGAG 7020
QY 7021 TCTGCGGAG 7080
Db 7021 TCTGCGGAG 7080
QY 7081 TCTGCGGAG 7140
Db 7081 TCTGCGGAG 7140
QY 7141 GAGGCTGAG 7200
Db 7141 GAGGCTGAG 7200

OY	7201	TCTGGGTCAGGCACATCATCATGTATPAGGCCACCCTGTGGGACAAGATATGATCCTGATG	7260
Dd	7201	TCTGGCTAGGCACATCATCATGTATGCGCCACCCTTGTGGCAAGATGATCCTGATG	7260
OY	7261	ACTCATTTCTTCATCATCTTCTAGCTCAGGAACAATTGAAAAAACCCTAGATTGTGACG	7320
Dd	7261	ACTCATTTCTTCATCATCTTCTTAGCTCAGGAACAACACTTGAAAAAGCCCTAGATTGTGACG	7320
OY	7321	ATTCACGGGGCCTTTCTACTCATTTAGGCCACTTGACCTFACCTCAGATCATTAACAGACTC	7380
Dd	7321	ATTCACGGGGCCTTTCTACTCATTTAGGCCACTTGACCTFACCTCAGATCATTAACAGACTC	7380
OY	7381	CATGGCCTTAGCCGATTTTCTACTCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
Dd	7381	CATGGCCTTAGCCGATTTTCTACTCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT	7440
OY	7441	TGATGSCCTCAGGAACATTGGGGGTACCGCCCTTGCGAGTGTGGAGACATGGGCCAGAACT	7500
Dd	7441	TGATGSCCTCAGGAACATTGGGGGTACCGCCCTTGCGAGTGTGGAGACATGGGCCAGAACT	7500
OY	7501	GTCGGCGCTTAGGCTACTGTGCCAGGGGGGAGGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
Dd	7501	GTCGGCGCTTAGGCTACTGTGCCAGGGGGGAGGGGCTGCCACTTGTGGCAAGTACCTCTTC	7560
OY	7561	AAC TGCGCAGTAAGAGACCAAGCTCAAAC TACTCCAAATCCGSGCTGGCTCCAGTGGAT	7620
Dd	7561	AAC TGCGCAGTAAGAGACCAAGCTCAAAC TACTCCAAATCCGSGCTGGCTCCAGTGGAT	7620
OY	7621	TTATCCAGCTTGATTCTGTCTGTTACAGCGGGGGAAGACATAATDACAAGCTGTCTGCT	7680
Dd	7621	TTATCCAGCTTGATTCTGTCTGTTACAGCGGGGGAAGACATAATDACAAGCTGTCTGCT	7680
OY	7681	GCCCGACCCCGCTGGTTCATGATGTCGCTACTCTACTTTCTGTAGGGGTAGGCAATCAT	7740
Dd	7681	GCCCGACCCCGCTGGTTCATGATGTCGCTACTCTACTTTCTGTAGGGGTAGGCAATCAT	7740
OY	7741	CTACTCCCCCAACCGATATAGCGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT	7800
Dd	7741	CTACTCCCCCAACCGATATAGCGGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT	7800
OY	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Dd	7801	TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
OY	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Dd	7861	TTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
OY	7921	TAGCTGTGAAGAAGTCCTGAGCCGCTTGATGACAGAGAGATGCTGATAGTGGCTCTTGCC	7980
Dd	7921	TAGCTGTGAAGAAGTCCTGAGCCGCTTGATGACAGAGAGATGCTGATAGTGGCTCTTGCC	7980
OY	7981	AGATCAGTACT 7992	
Dd	7981	AGATCAGTACT 7992	
RESULT 7			
ID	ALA47279	standard; DNA; 7991 bp.	
XX	XX	ALA47279;	
XX	XX	30-AUG-2002 (first entry)	
DE	HEPATITIS C VIRUS SUB-GENOMIC REPLICON RECOMBINANT CLONE HCV9.		
KX	HEPATITIS; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;		
KW	virulence; hepatotropic; gene therapy; anti-viral; gene; ds.		
OS	Hepatitis C virus.		
PIN	MO200238793-A2.		

XX 16-MAY-2002.
 PD
 XX 02-NOV-2001; 2001WO-US46350.
 PF
 XX 07-NOV-2000; 2000US-245866P.
 PR
 XX (ANAD-) ANADYS PHARM INC.
 PA
 XX Bichko V;
 PI
 XX
 DR WPI: 2002-490062/52.
 XX
 PT Novel nucleic acid encoding replication competent recombinant hepatitis
 PT C virus genome useful for screening anti-hepatitis C virus therapeutics
 PT and for vaccine development
 PS
 XX
 PS Claim 9: Page 61-65; 85pp; English.
 CC The present invention provides protein and coding sequences from
 CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
 CC able to replicate efficiently when transfected into a susceptible cell
 CC line without reducing the growth rate of the cell line by more than 10
 CC fold. The sequences are useful for screening for anti-HCV therapeutics,
 CC for detecting antibodies to HCV in a biological sample such as blood,
 CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
 CC for deriving authentic HCV components such as replication-complement
 CC non-infectious, replication-defective infection-component, and
 CC replication-defective non-infectious HCV, in gene therapy or gene
 CC vaccination targeted to hepatic tissue for treating an animal infected or
 CC susceptible to HCV infection and for studying HCV infection and
 CC propagation. The present sequence is a clone of a fragment of the HCV
 CC genome designated HCV99.
 CC
 XX
 SQ Sequence 7991 BP; 1647 A; 2369 C; 2245 G; 1730 T; 0 other:
 Query Match 99.8%; Score 7980; DB 24; Length 7991;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 7991; Conservative 0; Mismatches 0; Indels 1; Gaps 1
 QY 1 GCCAGCCCCCGATGTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACTACTG 60
 DB 1 GCCAGCCCCCGATGTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACTACTG 60
 QY 61 TCTTCAGGAGGAAGGCGTCTAGCCATGGGTTAGTATGATGATGCTGGAGCTCCAGAGAC 120
 DB 61 TCTTCAGGAGGAAGGCGTCTAGCCATGGGTTAGTATGATGATGCTGGAGCTCCAGAGAC 120
 QY 121 CCCCCTCCCGGAGAGGCCATAGTGGTTCGCGGAACCCGTAGTACACCGGAATTGGCCAG 180
 DB 121 CCCCCTCCCGGAGAGGCCATAGTGGTTCGCGGAACCCGTAGTACACCGGAATTGGCCAG 180
 QY 181 GAGCACCAGGGGTCTTCTTCTTGATCAACCCGCTCATGCTGAGATTTGGGCGTGGCCCC 240
 DB 181 GAGCACCAGGGGTCTTCTTCTTGATCAACCCGCTCATGCTGAGATTTGGGCGTGGCCCC 240
 QY 241 GCGAGACTGTAGCCACAGTAGTGTGGGATGCCGAAAGGCGTTGTGGTACTGCCATGAG 300
 DB 241 GCGAGACTGTAGCCACAGTAGTGTGGGATGCCGAAAGGCGTTGTGGTACTGCCATGAG 300
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 QY 361 CTCAGAGAAACCAAGGCGCGCCATGATATTGAACAAGATGGATTGCACGACAGTTCTC 420
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 QY 481 CTGATGCCCGCGCTGTTCGCGCTGTGACGCCACAGGGCGGCCGCGATTCTTTTGTCAAGACG 540


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QY 541 ACCCTTCGGGTGCGCTGTGATGAATGACGACGAGGCGAGCGGCTATCTGTGGCTGCCA 600
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Page 30

XX Hepatitis C virus (HCV) adaptive replicon V mutant cDNA.
 DE
 XX
 KM Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 KM gene therapy; vaccine; immunoprotection; hepatotropic; viraecide; liver;
 KM adaptive replicon V; mutant; ss.
 OS
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 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
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 FT /product= "NS5A variant of HCV adaptive replicon V"
 FT /note= "CDS does not include both start and stop
 FT codon"
 FT /partial
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 FT /tag= b
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 PF 23-MAY-2000; 2000US-0576989.
 PR
 PA (UNIV) UNIV WASHINGTON.
 XX
 XX Rice CM, Blight KJ;
 PI
 DR WPI: 2002-066755/09.
 DR P-PSDB: AAE15724.
 XX
 PT Hepatitis C virus variants having greater transfection efficiency and
 PT ability to survive subpassage, useful as a vaccine for immunizing
 PT primate to the virus, comprise non-naturally occurring viral sequences
 PT
 PS Disclosure; Page 80-83; 174pp; English.
 XX
 XX The invention relates to Hepatitis C virus (HCV) variants which include
 CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
 CC variants that have a transfection efficiency and ability to survive
 CC subpassage greater than HCV that have wild-type polypeptide coding
 CC regions. The polynucleotides of the invention are useful for identifying
 CC a cell line that is permissive for infection with HCV and detecting
 CC replication of HCV in cells of the cell line. They are also useful for
 CC testing a compound for anti-viral properties and for inhibiting HCV
 CC infection. They are also useful for the generation of defined HCV virus
 CC stocks to develop in vitro and in vivo assays for virus neutralisation,
 CC attachment, penetration and entry, structure/function studies on HCV
 CC proteins and RNA elements and identification of new antiviral targets,
 CC a systematic survey of cell culture systems and conditions to identify
 CC those that support wild-type and variant HCV RNA replication and
 CC particle release, production of adaptive HCV variants capable of more
 CC efficiency replication in cell culture, production of HCV variants with
 CC altered tissue or species tropism, establishment of alternative animal
 CC models for inhibitor evaluation including those supporting HCV variant
 CC replication, development of cell-free HCV replication assays.
 CC Production of immunogenic HCV particles for vaccination, engineering of
 CC attenuated HCV derivatives as possible vaccine candidates, engineering
 CC of attenuated or defective HCV derivatives for expression of
 CC heterologous gene products for gene therapy and vaccine applications
 CC and for utilisation of the HCV glycoproteins for targeted delivery of
 CC therapeutic agents to the liver or other cell types with appropriate
 CC receptors. Vaccine comprising these sequences is useful for inducing
 CC immunoprotection to HCV in a primate. The present sequence is
 CC Hepatitis C virus (HCV) adaptive replicon V mutant cDNA. This sequence
 CC is generated by the mutation g to t at position 5320 of
 CC HCVrep1bBartman/Avail cDNA.
 XX

SQ Sequence 7989 BP; 1647 A; 2369 C; 2241 G; 1732 T; 0 other;

Query Match 99.8%; Score 7979.4; DB 24; Length 7989;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 7983; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 1 GCCACCCCCCGATTGGGGGCGACACTGCACATATGATCTCCCTGTGAGAACTACTG 60
QY 61 TCTTACGACGAAACGCTAGCCATGGCGTTAGTATGATGATGTCGTGACACCTCCAGAC 120
DB 61 TCTTACGACGAAACGCTAGCCATGGCGTTAGTATGATGATGTCGTGACACCTCCAGAC 120
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DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTGCGAG 180
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DB 181 GACGACCGGGTCTTCTTGATCAACCCGCTCATGGCTGAGAGATTGGGCGTGCCTAAC 240
QY 241 GCGAGACTGTAGCCGAGTGTGTGGTCCGGAAGGCTTGTGTACTGTCTGATAGG 300
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 QY 6961 GCGGGGACCCAAAGAGACGAGGCGAGCTACGCGCTTACAGAGAGCTATGACTGATATC 7020
 DB 6961 GCGGGGACCCAAAGAGAGGAGCGAGGAGCTACGCGCTTACAGAGAGCTATGACTGATATC 7020
 QY 7021 TCTGCCCCCTTGGGAGACCGGCCCAAGCAGATACGACTTGGATTGATTAACATCATGCG 7080
 DB 7021 TCTGCCCCCTTGGGAGACCGGCCCAAGCAGATACGACTTGGATTGATTAACATCATGCG 7080
 QY 7081 TCCCTCCAACTGTTCAGTCGCGGACGATGATCTGGCAAAAGGTTACTATCTCCACCGCT 7140
 DB 7081 TCCCTCCAACTGTTCAGTCGCGGACGATGATCTGGCAAAAGGTTACTATCTCCACCGCT 7140
 QY 7141 GACCCGACACACCCCTTGGCGGGGCTGTGGAGACAGCTAGACACCTCCAGTCAAT 7200
 DB 7141 GACCCGACACACCCCTTGGCGGGGCTGTGGAGACAGCTAGACACCTCCAGTCAAT 7200
 QY 7201 TCCCTGCTAGGCAACATCATGATGTGCGCCACCTTGTGGGCAAGATGATCCTGATG 7260
 DB 7201 TCCCTGCTAGGCAACATCATGATGTGCGCCACCTTGTGGGCAAGATGATCCTGATG 7260
 QY 7261 ACTCATTTCTTCCATCTCTTCTAGCTCAGGAACAACCTTGAAGAAAGCCCTAGATTGTGAG 7320
 DB 7261 ACTCATTTCTTCCATCTCTTCTAGCTCAGGAACAACCTTGAAGAAAGCCCTAGATTGTGAG 7320
 QY 7321 ATCTACGGGCGCTGTACTACTGATGAGCCACTTACCTTACATGATCTTCAAGACTG 7380
 DB 7321 ATCTACGGGCGCTGTACTACTGATGAGCCACTTACCTTACATGATCTTCAAGACTG 7380
 QY 7381 CATGGCCTTAGCGATTTTACTCCATAGTACTCTCCAGGTAGATCAATAGGCTGTGCT 7440
 DB 7381 CATGGCCTTAGCGATTTTACTCCATAGTACTCTCCAGGTAGATCAATAGGCTGTGCT 7440
 QY 7441 TCATGCTCAGGAAACTTGGGGTACCGCCCTTGGAGTGTGAGAAATGCGGCCAGAGT 7500
 DB 7441 TCATGCTCAGGAAACTTGGGGTACCGCCCTTGGAGTGTGAGAAATGCGGCCAGAGT 7500
 QY 7501 GTCCGCGCTAGGCTACTGTCTCCAGGGGGAGGGGCTGACACTTGTGCAAGTACTCTTC 7560
 DB 7501 GTCCGCGCTAGGCTACTGTCTCCAGGGGGAGGGGCTGACACTTGTGCAAGTACTCTTC 7560
 QY 7561 AACTGGGAGTAAAGACCAAGTCAAACTCACTCCAAATCCCGGCTCGTCCCAAGTTGAT 7620

DB 7561 AACTGGGAGTAAAGACCAAGCTCAAACTCACTCAATCCCGGCTGGCTCCAGATTGAT 7620
 QY 7621 TTAATCAGCTGTGCTGTGCTGTGTACAGCGGGGAGACATATATACAGGCTGTCTGCT 7680
 DB 7621 TTAATCAGCTGTGCTGTGCTGTGTACAGCGGGGAGACATATATACAGGCTGTCTGCT 7680
 QY 7681 GCCCGACCCCGCTGTTTCTATGTGTGCTACTCTACTTCTGTAGGGGTAGGATCTAT 7740
 DB 7681 GCCCGACCCCGCTGTTTCTATGTGTGCTACTCTACTTCTGTAGGGGTAGGATCTAT 7740
 QY 7741 CTACTCCCAACCGATGAAGCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTT 7800
 DB 7741 CTACTCCCAACCGATGAAGCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTT 7800
 QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 DB 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 QY 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
 DB 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
 QY 7921 TAGCTGTGAAGGTCCGTGAGCGCGCTTGAAGTGAAGATGCTGATGCTGCTGCTG 7980
 DB 7921 TAGCTGTGAAGGTCCGTGAGCGCGCTTGAAGTGAAGATGCTGATGCTGCTGCTGCTG 7980
 QY 7981 AGATCAAGT 7989
 DB 7981 AGATCAAGT 7989

RESULT 9
 ID AAD25325 standard: cDNA; 7989 BP.
 AC AAD25325;
 DT 12-MAR-2002 (first entry)
 XX
 DE Hepatitis C virus (HCV) adaptive replicon II cDNA mutant.
 XX
 KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 KW gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
 KW adaptive replicon II; mutant; ss.
 OS Hepatitis C virus.
 OS Synthetic.
 FH key location/Qualifiers
 FT CDS 1801..7758
 FT /tag= a "HCV adaptive replicon II protein"
 FT /product= b
 FT /tag= b
 FT /product= "NS5a protein of HCV adaptive replicon II"
 FT /note= "CDS does not include both start and stop
 FT codon"
 FT /partial
 PN MO200189364-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001: 2001MO-US16822.
 XX
 PR 23-MAY-2000: 2000US-0576989.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Rice CM, Blight KJ;
 XX
 DR WPI; 2002-066755/09.

DR P-PSDB; AAE15722, AAE15723.

PT Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences
PT

Example 1; Page 77-80; 174pp; English.

CC The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop *in vitro* and *in vivo* assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets,
CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficient replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays,
CC production of immunogenic HCV particles for vaccination, engineering of
CC attenuated HCV derivatives as possible vaccine candidates, engineering
CC of attenuated or defective HCV derivatives for expression of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) adaptive replicon II cDNA mutant. This sequence
CC is generated by the mutation a to g at position 5289 of
CC HCVrepBartman/Vaili cDNA.

Sequence 7989- BP; 1644 A; 2369 C; 2245 G; 1731 T; 0 other;

Query Match	99.8%;	Score 7976.2;	DB 24;	Length 7989;
Best Local Similarity	99.9%;	Pred. No. 0;		

Matches 7981; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	1	GGCGAGCCCCGATTTGGGGGGCCACACTCCACCATATGATCACTCCCTCTGTGAGAACACTG	60
Db	1	GGCAGGCCCCGATTTGGGGGGCCACACTCCACCATATGATCACTCCCTCTGTGAGAACACTG	60
QY	61	TCTTCAGCAGAAACGCTCTAGCCATGAGCGCTTGATATGATGTCGGTCGGAGCCCTCAGGAC	120
Db	61	TCTTCAGCAGAAACGCTCTAGCCATGAGCGCTTGATATGATGTCGGTCGGAGCCCTCAGGAC	120
QY	121	CCCCCTCCCGGGAGAGCCATAGTGTCTCGGAGACCGGTGAGTACACCGAATTTGCCAG	180
Db	121	CCCCCTCCCGGGAGAGCCATAGTGTCTCGGAGACCGGTGAGTACACCGAATTTGCCAG	180
QY	181	GAGGACCGGGTCTTTCTTGGATATACCCCGCTCAATGCTCGAGATTTTGGCGTGGCCCC	240
Db	181	GAGGACCGGGTCTTTCTTGGATATACCCCGCTCAATGCTCGAGATTTTGGCGTGGCCCC	240
QY	241	GGCAGACTCTAGCCGAGTATGTTGGGTGGCGAAAGGCGCTGTGGTACTGCGTATAGG	300
Db	241	GGCAGACTCTAGCCGAGTATGTTGGGTGGCGAAAGGCGCTGTGGTACTGCGTATAGG	300
QY	301	GTCGTTGGCAGTGGCCCCGGGAGAGTCTGTGAGACCGTGCACCATGAGCAGATCTTAAC	360
Db	301	GTCGTTGGCAGTGGCCCCGGGAGAGTCTGTGAGACCGTGCACCATGAGCAGATCTTAAC	360
QY	361	CTCAAGAAACAAAGGGCGCCGCTGATATTAACAATAATGATTTGCACGCAAGTTC	420
Db	361	CTCAAGAAACAAAGGGCGCCGCTGATATTAACAATAATGATTTGCACGCAAGTTC	420

OY	421	CGCGCGCTTGGGTGAGAGGCTATTCTGGCGATATGACGTGGCGACAAACGAAATCGGCTCT	480
Db	421	CGCGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGACACAGACAAATCGGCTGT	480
OY	481	CTGATGCCGCCGTCTTCGCGGCTGTCAAGCGAGAGGGGCCCGCGTCTTTTGTCAAGACCG	540
Db	481	CTGATGCCGCCGTCTTCGCGGCTGTCAAGCGAGAGGGGCCCGCGTCTTTTGTCAAGACCG	540
OY	541	ACCGTCCGGGTGGCCCTGAATGAACGTGAGAGACAGAGGACAGGGGCGATATGTTGGCTGGCCA	600
Db	541	ACCGTCCGGGTGGCCCTGAATGAACGTGAGAGACAGAGGACAGGGGCGATATGTTGGCTGGCCA	600
OY	601	CGACGGGCGTTCCTTGGCGACGCTGTGTCAGCTTGTCACTGAAGCGGGAGAGGACTGAC	660
Db	601	CGACGGGCGTTCCTTGGCGACGCTGTGTCAGCTTGTCACTGAAGCGGGAGAGGACTGAC	660
OY	661	TGCTATTGGGGGAAGTCCCGGGGAGGAGTCTCTGTCACTCACTCACTCACTGGCTCCGCGAGA	720
Db	661	TGCTATTGGGGGAAGTCCCGGGGAGGAGTCTCTGTCACTCACTCACTCACTGGCTCCGCGAGA	720
OY	721	AAGTATCCATCATGCTGTATGATCAATGGCGGCGCTGCATACGCTTGATCCGCGCTACCTGCC	780
Db	721	AAGTATCCATCATGCTGTATGATCAATGGCGGCGCTGCATACGCTTGATCCGCGCTACCTGCC	780
OY	781	CATTGCACACCAAGCGCAAACTGCATGCATGAGGACAGCTACTCGGATGAGAGCGCGGTC	840
Db	781	CATTGCACACCAAGCGCAAACTGCATGCATGAGGACAGCTACTCGGATGAGAGCGCGGTC	840
OY	841	TTGTGATCAGATGATGTGGAGCAAGACATCAGGGGCTCGCGCCAGCGCACTGTTCC	900
Db	841	TTGTGATCAGATGATGTGGAGCAAGACATCAGGGGCTCGCGCCAGCGCACTGTTCC	900
OY	901	CCAGGCTCAAGGCGCGCATCCGAGCGGGAGATGTGTTGMACCCATGGCGCATGTGCT	960
Db	901	CCAGGCTCAAGGCGCGCATCCGAGCGGGAGATGTGTTGMACCCATGGCGCATGTGCT	960
OY	961	GCTTGGCGAATATCATGTGGTGAANAATGGCCGCTTTTCTGGAATCATGACTGTGGCGGC	1020
Db	961	GCTTGGCGAATATCATGTGGTGAANAATGGCCGCTTTTCTGGAATCATGACTGTGGCGGC	1020
OY	1021	TGGGTGTGGCGGACCGGTATTCAGACATACCGTTGGCTACCCGTATATGTGTTGAAGAGC	1080
Db	1021	TGGGTGTGGCGGACCGGTATTCAGACATACCGTTGGCTACCCGTATATGTGTTGAAGAGC	1080
OY	1081	TTGGCGGCGAATGGGCTGACCGCTTCTCTGTGCTTTAGGGTATGCGCGCTCCCGATTGCG	1140
Db	1081	TTGGCGGCGAATGGGCTGACCGCTTCTCTGTGCTTTAGGGTATGCGCGCTCCCGATTGCG	1140
OY	1141	AGGCGATGCGCTTATTCGCGCTTCTTGAAGAGTCTTTCAGTTTAAAGACAGCCAGAGC	1200
Db	1141	AGGCGATGCGCTTATTCGCGCTTCTTGAAGAGTCTTTCAGTTTAAAGACAGCCAGAGC	1200
OY	1201	GTTTCCCTCTAGGCGGATCAATTCCGCGCTCTCCCTCCCCCCCCCTTACGTTACTGGC	1260
Db	1201	GTTTCCCTCTAGGCGGATCAATTCCGCGCTCTCCCTCCCCCCCCCTTACGTTACTGGC	1260
OY	1261	CGAAGCGCGCTTGAATTAAGCGCGGTGTGGTGTGTATATTTAAATTCACCATATTG	1320
Db	1261	CGAAGCGCGCTTGAATTAAGCGCGGTGTGGTGTGTATATTTAAATTCACCATATTG	1320
OY	1321	CCGTCCTTTTGGCAATGTGAAGGCGCGGAAACCTGGCCCTGTCTTGTGAAGAGCACTTCT	1380
Db	1321	CCGTCCTTTTGGCAATGTGAAGGCGCGGAAACCTGGCCCTGTCTTGTGAAGAGCACTTCT	1380
OY	1381	AGGAGGTCTTTCCTCTCCGCGCAAGAATGCAAGGCTCTTAAATGTGTTGAAGAACA	1440
Db	1381	AGGAGGTCTTTCCTCTCCGCGCAAGAATGCAAGGCTCTTAAATGTGTTGAAGAACA	1440
OY	1441	GTTCTCTGTGAAGCTTCTTGAAGACAACACGCTCTGTAGCAGCCCTTTGCAAGCAGCGG	1500
Db	1441	GTTCTCTGTGAAGCTTCTTGAAGACAACACGCTCTGTAGCAGCCCTTTGCAAGCAGCGG	1500

QY	1501	AA	CCCCCACCCTGGCGACAGAGTGCCTCTCGGGCCAAANAACCGCTGTAAATGATACACT	1560
Db	1501	AA	CCCCCACCCTGGCGACAGAGTGCCTCTCGGGCCAAANAACCGCTGTAAATGATACACT	1560
QY	1561	GCA	AGGCGGGACACACCCCAAGTGCACAGTGTGAGTATGTTGTGGAAGAAGTCAAA	1620
Db	1561	GCA	AGGCGGGACACACCCCAAGTGCACAGTGTGAGTATGTTGTGGAAGAAGTCAAA	1620
QY	1621	TGG	CTCTCCATCAAGCGATTAACAACAGGGGGGTGAAGGAAATGCCCAAGTACCCCATTTGT	1680
Db	1621	TGG	CTCTCTCCATCAAGCGATTAACAACAGGGGGGTGAAGGATGCCCAAGAGTACCCCATTTGT	1680
QY	1681	ATG	GGATCTGATCTGGGGCCCTCGGTGCACATGCTTTACATGTTTAATCGAGGTTAAA	1740
Db	1681	ATG	GGATCTGATCTGGGGCCCTCGGTGCACATGCTTTACATGTTTAATCGAGGTTAAA	1740
QY	1741	AAC	CTTAGGCCCCCGCAACACAGGGGAGTGTGTTTCTTTGAAAACACAGATATATAC	1800
Db	1741	AAC	CTTAGGCCCCCGCGAACAACAGGGGAGTGTGTTTCTTTGAAAACACAGATATATAC	1800
QY	1801	ATG	CGCCCTATTAGGCGCTACTCCCAACAGAGCGAGCGCTACTTGCTGTCATCATCACT	1860
Db	1801	ATG	CGCGCCCTATTAGGCGCTACTCCCAACAGAGCGAGCGCTACTTGCTGTCATCATCACT	1860
QY	1861	AGC	CTCAGAGCGGGACAGACACAGATCGAAGGGGAGAGTCAAGTGTGTCCACGGCA	1920
Db	1861	AGC	CTCAGACAGAGCGGGACAGACACAGATCGAAGGGGAGAGTCAAGTGTGTCCACGGCA	1920
QY	1921	ACACA	NTTCTCTGGCGACCTGCTCAATGGCGTGTGTGAGCTGTCTATCATATGTGTCC	1980
Db	1921	ACACA	NTTCTCTGGCGACCTGCTCAATGGCGTGTGTGAGCTGTCTATCATATGTGTCC	1980
QY	1981	GGC	TCAAGAAGACCTTGGCGGCCCAAGAGGGCCCAATCACCAATTTAACCANAATGTGAC	2040
Db	1981	GGC	TCAAGAAGACCTTGGCGGCCCAAGAGGGCCCAATCACCAATTTAACCANAATGTGAC	2040
QY	2041	CAG	ACTCGTGGGTGAGAGCGCCCCCGGGGGCGCTTCTTATCAACATGCACACTGAC	2100
Db	2041	CAG	ACTCGTGGGTGAGAGCGCCCCCGGGGGCGCTTCTTATCAACATGCACACTGAC	2100
QY	2101	GGC	AGCTCGGACCTTACTTGTGCAGAGGCAATGCGATGATTCGCGTGGCGGGGG	2160
Db	2101	GGC	AGCTCGGACCTTACTTGTGCAGAGGCAATGCGATGATTCGCGTGGCGGGGG	2160
QY	2161	GGG	CACAGAGGGGAGGACCTACTCTCCCCAGGGCCGCTCTCTACTTGAAGGGCTTTGC	2220
Db	2161	GGG	CACAGAGGGGAGGACCTACTCTCCCCAGGGCCGCTCTCTACTTGAAGGGCTTTGC	2220
QY	2221	GGG	GGTCCACTGCTCTGCCCCCTGGGGGCAACGCTGTGGGCATTTTCGGGGCTGTGC	2280
Db	2221	GGG	GGTCCACTGCTCTGCCCCCTGGGGGCAACGCTGTGGGCATTTTCGGGGCTGTGC	2280
QY	2281	ACC	GAGGGGGTGGGAAGGGGGTGGACCTTGTAAACCGTGTGATGTGAAGAAACAATAAG	2340
Db	2281	ACC	GAGGAGGGGGTGGGAAGGGGGTGGACCTTGTAAACCGGTGTGATGTGAAGAAACAATAAG	2340
QY	2341	CGG	TCCCGGCTTTCACGAGCAACAATCGTCCCTCGGGCCGTAACCGCAGACATTCAGGTG	2400
Db	2341	CGG	TCCCGGCTTTCACGAGCAACAATCGTCCCTCGGGCCGTAACCGCAGACATTCAGGTG	2400
QY	2401	GCC	ATCTACAGGGCCCTTATGTGTATAGCGGAAGAGACTAAAGTGCAGGCTGTGCGATGCA	2460
Db	2401	GCC	ATCTACAGCGCCCTTACTGTGTATAGCGGAAGAGACTAAAGTGTCCGGCTGTGATGCA	2460
QY	2461	GCC	CAAGGATTAAGGATGTGTCTGAAACCGGTCCGTCGCCGACACCTTAGGTTTCGGG	2520
Db	2461	GCC	CAAGGATTAAGGATGTGTCTGAAACCGGTCCGTCGCCGACACCTTAGGTTTCGGG	2520
QY	2521	GCG	ATATGTCTAAAGGACATGTGTATCGAACCTTAACATAGAACCGGGGTAAAGGACATC	2580
Db	2521	GCG	ATATGTCTTAAGGACATGTGTATCGAACCTTAACATAGAACCGGGGTAAAGGACATC	2580
QY	2581	ACA	CGGGGTCCCCCATCAGTACTCCACTATGGCAGAGTTTCTTCCGAGCGGTGTGTC	2640

Db	2551	ACACGGGTGCCCCCATCAGCTACTCCACCTATGGAAATTTCTTGCCGAGGTGTGTC	2640
Qy	2641	TCGTGGGGCGCCTATGACATCATATAATGATGAGTGGCACTCACTGACTCGACACT	2700
Db	2641	TCGTGGGGCGCCTATGACATCATATAATGATGAGTGGCACTCACTGACTCGACACT	2700
Qy	2701	ATCCGGGGCAATCGGCACAGTCTGTGGACAAAGCGAGAGCGGTGGAGCGGACTGCTGTG	2760
Db	2701	ATCCGGGGCAATCGGCACAGTCTGTGGACAAAGCGAGAGCGGTGGAGCGGACTGCTGTG	2760
Qy	2761	CTCGCCACCGCTACGCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGAGGTG	2820
Db	2761	CTCGCCACCGCTACGCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGAGGTG	2820
Qy	2821	GCTGTGTCACCACTGAGAAATCCCTTTATGGAAGAACATCCCATCGAGACATC	2880
Db	2821	GCTGTGTCACCACTGAGAAATCCCTTTATGGAAGAACATCCCATCGAGACATC	2880
Qy	2881	AAGGGGGGAGGACCTCATTTTCTGCGATTCCAGAGAAATGTGATGAGCTGGCGCG	2940
Db	2881	AAGGGGGGAGGACCTCATTTTCTGCGATTCCAGAGAAATGTGATGAGCTGGCGCG	2940
Qy	2941	AAGCTGTCCGGCCCTCGGAGCAATGCTGTGATTAATTCAGGGGCGTTGATATCCGTC	3000
Db	2941	AAGCTGTCCGGCCCTCGGAGCAATGCTGTGATTAATTCAGGGGCGTTGATATCCGTC	3000
Qy	3001	ATACCACTAGCGAGACGTCATTTGTGTGACAGCGACGCTCTATATGACGGGCTTTAC	3060
Db	3001	ATACCACTAGCGAGACGTCATTTGTGTGACAGCGACGCTCTATATGACGGGCTTTAC	3060
Qy	3061	GAGCGATTCGAGTCAGATGATCGAGTCGTAATACATGTGTACACCAACAGTCGACTACG	3120
Db	3061	GAGCGATTCGAGTCAGATGATCGAGTCGTAATACATGTGTACACCAACAGTCGACTACG	3120
Qy	3121	CTGGACCCGACCTTCACCATTTAGAGAGAGAGACCGCTGCCAAGAGCGCGTGTACAGCTCG	3180
Db	3121	CTGGACCCGACCTTCACCATTTAGAGAGAGAGACCGCTGCCAAGAGCGCGTGTACAGCTCG	3180
Qy	3181	CAGCGGCGAGGACAGAGACTGATAGGGGAGAGATGGGATTTAAGGTTTGTGACTCCAGA	3240
Db	3181	CAGCGGCGAGGACAGAGACTGATAGGGGAGAGATGGGATTTAAGGTTTGTGACTCCAGA	3240
Qy	3241	GAAAGCGCCCTGGGCAATGTCGAAATCTCGGTCTGTGGAGATGCGATATGAGCGCGGCGT	3300
Db	3241	GAAAGCGCCCTGGGCAATGTCGAAATCTCGGTCTGTGGAGATGCGATATGAGCGCGGCGT	3300
Qy	3301	GCTTGTGACGAGCTCACGCGCCGCGGAGACCTCAGTTAGTTGCGGGCTTAACCTAAACACA	3360
Db	3301	GCTTGTGACGAGCTCACGCGCCGCGGAGACCTCAGTTAGTTGCGGGCTTAACCTAAACACA	3360
Qy	3361	CGAGGTTGGCCCGTCTGCGAGAGACATCTGGAATTTGGGAGAGCGTCTTTACAGCCCTC	3420
Db	3361	CGAGGTTGGCCCGTCTGCGAGAGACATCTGGAATTTGGGAGAGCGTCTTTACAGCCCTC	3420
Qy	3421	ACCCACATAGAGCCCAATTTCTTGTGCCAGACTAAGCAGGCAAGAGACAATTCCTCCCTAC	3480
Db	3421	ACCCACATAGAGCCCAATTTCTTGTGCCAGACTAAGCAGGCAAGAGACAATTCCTCCCTAC	3480
Qy	3481	CTGGAGATATCCAGGCTACGAGTGTGGGCGCAGGAGCTCAAGCTCACTCATCTGGGAGC	3540
Db	3481	CTGGAGATATCCAGGCTACGAGTGTGGGCGCAGGAGCTCAAGCTCACTCATCTGGGAGC	3540
Qy	3541	CAATGTGAGAGTGTCTCATACGGCTAAGGCTACGCTCCAGGGCAACGCCCTCTGCTG	3600
Db	3541	CAATGTGAGAGTGTCTCATACGGCTAAGGCTACGCTCCAGGGCAACGCCCTCTGCTG	3600
Qy	3601	TATAGCTGGAGACGCTTCAAAAGAGAGTTACTACACACACCCCATAAACAAATATATC	3660
Db	3601	TATAGCTGGAGACGCTTCAAAAGAGAGTTACTACACACACCCCATAAACAAATATATC	3660
Qy	3661	ATGGCATGATGTGCGCTGACCTGGAGGTCGTACAGACGACCTGGGTGCTGTAGCGGA	3720
Db	3661	ATGGCATGATGTGCGCTGACCTGGAGGTCGTACAGACGACCTGGGTGCTGTAGCGGA	3720

Db	3661	ATGSCATGATGTCGCGTACCTGACCTGGAGAGTGTGCACAGACCACTGGGTGCTGTGAGGCGGA	3712
OY	3721	GTCCTACGACGCTGGCCCGCTATTGCTCTGACACAGCAGCGTGTGTCATTGTGGGAGG	3780
Db	3721	GTCCTACGACGCTGGCCCGCTATTGCTCTGACACAGCAGCGTGTGTCATTGTGGGAGG	3780
OY	3781	ATCATCTTGTCCGGAAGGCGGCGCATCTTCCCGACAGGGAAGTCTTTACCGGGAATTC	3840
Db	3781	ATCATCTTGTCCGGAAGGCGGCGCATCTTCCCGACAGGGAAGTCTTTACCGGGAATTC	3840
OY	3841	GATAGATGGAAGAGTGGCCTTACACCTCTCCCTTACATTCGAACAGGGAATGCACCTGGC	3900
Db	3841	GATAGATGGAAGAGTGGCCTTACACCTCTCCCTTACATTCGAACAGGGAATGCACCTGGC	3900
OY	3901	GACCAATTCAACAGAAAGGCAATCGGGTGTGTCGAACAGCACCACAACAGCGAGAGCT	3960
Db	3901	GACCAATTCAACAGAAAGGCAATCGGGTGTGTCGAACAGCACCACAACAGCGAGAGCT	3960
OY	3961	GCTGCTCCCTGGTGGATTCAGTAGTGGCGGACCCTTCGAAGCTTCTGGGCGCAACATATG	4020
Db	3961	GCTGCTCCCTGGTGGATTCAGTAGTGGCGGACCCTTCGAAGCTTCTGGGCGCAACATATG	4020
OY	4021	TGCATTTTCATCAGCGGATACAAATATTAGCAGGCTTCCACTCTCCTCGCAACCCC	4080
Db	4021	TGCATTTTCATCAGCGGATACAAATATTAGCAGGCTTCCACTCTCCTCGCAACCCC	4080
OY	4081	GCGATAGCATCTGATGGCATTCACAGCCTCTATTCACAGCCGCTTACCACCCAACT	4140
Db	4081	GCGATAGCATCTGATGGCATTCACAGCCTCTATTCACAGCCGCTTACCACCCAACT	4140
OY	4141	ACCCTCGTATTAACTCCGCGGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCCAAGGCT	4200
Db	4141	ACCCTCGTATTAACTCCGCGGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCCAAGGCT	4200
OY	4201	GCTTCTGTTTCGTAAGCGCGCGGCATTCGCTGAGAGCGGCTGTGGAGATAGGCTTGGG	4260
Db	4201	GCTTCTGTTTCGTAAGCGCGCGGCATTCGCTGAGAGCGGCTGTGGAGATAGGCTTGGG	4260
OY	4261	AAGGTGCTGTGTGATATATTTTGGCAGGTTATGAGCAGGAGGTGGCAGGCGCTCGTGGCC	4320
Db	4261	AAGGTGCTGTGTGATATATTTTGGCAGGTTATGAGCAGGAGGTGGCAGGCGCTCGTGGCC	4320
OY	4321	TTTAAGTCATGAGCGCGCGAGATGCCCTCCACAGAGACCTGGCATCTACTCCCTGCT	4380
Db	4321	TTTAAGTCATGAGCGCGCGAGATGCCCTCCACAGAGACCTGGCATCTACTCCCTGCT	4380
OY	4381	ATCCTCTCCCTGGCGCCCTAGTGTGTCGGGGGTGTGTGCGCAGGATACTGCTGGGCAC	4440
Db	4381	ATCCTCTCCCTGGCGCCCTAGTGTGTCGGGGGTGTGTGCGCAGGATACTGCTGGGCAC	4440
OY	4441	GTCGGGCCAGGAGGAGGGGGCTGTGCATGTGATTAACCGGCTATATAGCGTTCGGCTTGGGG	4500
Db	4441	GTCGGGCCAGGAGGAGGGGGCTGTGCATGTGATTAACCGGCTATATAGCGTTCGGCTTGGGG	4500
OY	4501	GCTAAACAGTCTCCCGCAGCAGCACTATGTGCTGAGAGCGAGCGCTGCACAGCTGTCTACT	4560
Db	4501	GCTAAACAGTCTCCCGCAGCAGCACTATGTGCTGAGAGCGAGCGCTGCACAGCTGTCTACT	4560
OY	4561	CAGATCCCTCTAGCTTACCATCACTCACTGCTGAAGAGCTTCACACAGTGGATTCAC	4620
Db	4561	CAGATCCCTCTAGCTTACCATCACTCACTGCTGAAGAGCTTCACACAGTGGATTCAC	4620
OY	4621	GAGGACTGCTCCACGCCATGCTCCGCTGTGCTAAGAGATGTTTGGGATTTGGATATGC	4680
Db	4621	GAGGACTGCTCCACGCCATGCTCCGCTGTGCTAAGAGATGTTTGGGATTTGGATATGC	4680
OY	4681	ACGGGTGTGACTGATTTTCAAAACCTGGCTCACTCAACACTCCTGCGCGATTGCGGGGA	4740
Db	4681	ACGGGTGTGACTGATTTTCAAAACCTGGCTCACTCAACACTCCTGCGCGATTGCGGGGA	4740
OY	4741	GTCCTCTTCTTCATGTCAACGTGGGTACAAAGGAGTGTGGCGGGGCGACGGCATATG	4800
Db	4741	GTCCTCTTCTTCATGTCAACGTGGGTACAAAGGAGTGTGGCGGGGCGACGGCATATG	4800

QY	4801	CACACACACCTGCCCATGTGGAGCAGACGATCACCGGACATGTGAAAAGAGTTCATAGC	4866
Db	4801	CAAAACCACTTGCCCATATGTGGAGCAGACGATCACCGGACATGTGAAAAGAGTTCATAGC	4860
QY	4861	ATCTGTGGGGCCTTAGGACCTGTGTACTAACACAGTGGCATGTGAAACATTTCCCATTAACGCCTAC	4920
Db	4861	ATCTGTGGGGCCTTAGGACCTGTGTACTAACACAGTGGCATGTGAAACATTTCCCATTAACGCCTAC	4920
QY	4921	ACCAACGGGGCCCTGACAGCCCTCCCGGGGGCCAAATTTATCTAGGGCCCTGTGGCGGGTG	4980
Db	4921	ACCAACGGGGCCCTGACAGCCCTCCCGGGGGCCAAATTTATCTAGGGCCCTGTGGCGGGTG	4980
QY	4981	GCTGCTGAGGAGTAGTAGTGAGAGTTTACGGGGGTTGGGGGATTTTCAGCTACGTAGCGGCATG	5040
Db	4981	GCTGCTGAGGAGTAGTAGTGAGAGTTTACGGGGGTTGGGGGATTTTCAGCTACGTAGCGGCATG	5040
QY	5041	ACCACTGACACAGTAAGTCCCGCTGTCAAGTTCCGGCCCCCGAATTTCTTACAGAAAGTG	5100
Db	5041	ACCACTGACACAGTAAGTCCCGCTGTCAAGTTCCGGCCCCCGAATTTCTTACAGAAAGTG	5100
QY	5101	GATGGGCTGGCGTTGACAGAGTAGCGTCCAGAGGTGCAAAACCCCTCTTACGGGAGAGATC	5160
Db	5101	GATGGGCTGGCGTTGACAGAGTAGCGTCCAGAGGTGCAAAACCCCTCTTACGGGAGAGATC	5160
QY	5161	ACATTTCTGGTGGGCTCAATCAATACCTGTGTTGGTGCACAGCTCCCATGGAGCCCGAA	5220
Db	5161	ACATTTCTGGTGGGCTCAATCAATACCTGTGTTGGTGCACAGCTCCCATGGAGCCCGAA	5220
QY	5221	CCGGACGTAAGAGTGCCTCACTTCCATGCTACAGCAGCCCTCCACATTAACGGCGAGACG	5280
Db	5221	CCGGACGTAAGAGTGCCTCACTTCCATGCTACAGCAGCCCTCCACATTAACGGCGAGACG	5280
QY	5281	GCTAAGCGTAGAGCTGGCCAGAGGATCTCCGCCCTCTTGTGGCAGCTACTATCAGCTAGACG	5340
Db	5281	GCTAAGCGTAGAGCTGGCCAGAGGATCTCCGCCCTCTTGTGGCAGCTACTATCAGCTAGACG	5340
QY	5341	CTGTGTGGGCTTCTCTTGAAGGCAACATGACTACCCCTGATGACTGCCCGGAGCGTAGC	5400
Db	5341	CTGTGTGGGCTTCTCTTGAAGGCAACATGACTACCCCTGATGACTGCCCGGAGCGTAGC	5400
QY	5401	CTCATTCGAGGCCAACCTCTGTGGCGGACAGAAATGTGGGGGAAATACACCCCGGTGAG	5460
Db	5401	CTCATTCGAGGCCAACCTCTGTGGCGGACAGAAATGTGGGGGAAATACACCCCGGTGAG	5460
QY	5461	TCAGAAATTAAGTAGTAGTAATTTTGGACTTTTGAGCTCTTGACGCCCTCCAAAGCGAGAGATGAG	5520
Db	5461	TCAGAAATTAAGTAGTAGTAATTTTGGACTTTTGAGCTCTTGAGCGCCTCCAAAGCGAGAGATGAG	5520
QY	5521	AGGGAAGTAGTCCGTTCCGGCGGAGATCTGTGGAGTCTCAGAGAAATTCCTCTGACCGTAGT	5580
Db	5521	AGGGAAGTAGTCCGTTCCGGCGGAGATCTGTGGAGTCTCAGAGAAATTCCTCTGACCGTAGT	5580
QY	5581	CCCATATGAGGACCCCGGATTAACAACCTCCACTTTAGATCTCTGAGAGACCCGAGAC	5640
Db	5581	CCCATATGAGGACCCCGGATTAACAACCTCCACTTTAGATCTCTGAGAGACCCGAGAC	5640
QY	5641	TACGTCCCTCCAGTGTGTAACAAGGAGTGTCATTGGCCCTTGCCAAAGGCCCTCCCATACCA	5700
Db	5641	TACGTCCCTCCAGTGTGTAACAAGGAGTGTCATTGGCCCTTGCCAAAGGCCCTCCCATACCA	5700
QY	5701	CCTTCAGGAGAGAGAGAGAGAGTGTGCTCTCAGAAATCAACGTGTCTTCTCCCTTGGCG	5760
Db	5701	CCTTCAGGAGAGAGAGAGAGAGTGTGCTCTCAGAAATCAACGTGTCTTCTCCCTTGGCG	5760
QY	5761	GAGCTCGCCACAAGACCTTGTGGAGTCCGAATGTGTCCGCGGTGACACAGCGGACGSCA	5820
Db	5761	GAGCTCGCCACAAGACCTTGTGGAGTCCGAATGTGTCCGCGGTGACACAGCGGACGSCA	5820
QY	5821	ACGGCTCTCTCCGACAGACCCCTCCGAGAGAGGAGGAGGATCCGAGCTTAGTGTAGCTATAC	5880
Db	5821	ACGGCTCTCTCTCCGACAGACCCCTCCGAGAGAGGAGGAGGATCCGAGCTTAGTGTAGCTATAC	5880

QY	5881	TCCTCCATGCCCCCCTTGAGGGGAGAGCCGGGGATCCCGATCTCAGAGAGGGCTTGG	5941
Db	5881	TCCTCCATGCCCCCCTTGAGGGGAGAGCCGGGGATCCCGATCTCAGAGAGGGCTTGG	5940
QY	5941	TCCTACCGTAAGCGAGAGGCTAGTAGAGACGTGCTGCTGCTGATGTCTCTACACATGG	6000
Db	5941	TCCTACCGTAAGCGAGAGGCTAGTAGAGACGTGCTGCTGCTGATGTCTCTACACATGG	6000
QY	6001	ACAGAGCCCCCGATCAGCGCCATCGCTGGGAGAGAAACCAACTGTCGCATTAATGACATG	6060
Db	6001	ACAGAGCCCCCGATCAGCGCCATCGCTGGGAGAGAAACCAACTGTCGCATTAATGACATG	6060
QY	6121	CTGGGGGAGAAGAGGTGACACCTTTGACAGAGCTGACAGTCTTGAGAGACACTACCGGAG	6180
Db	6121	CTGGGGGAGAAGAGGTGACACCTTTGACAGAGCTGACAGTCTTGAGAGACACTACCGGAG	6180
QY	6181	GTGCTCAAGGAGATGAAGGCGAAGGCGCTCCACATTAAAGCTTAATCTTCATCCGTGGAG	6240
Db	6181	GTGCTCAAGGAGATGAAGGCGAAGGCGCTCCACATTAAAGCTTAATCTTCATCCGTGGAG	6240
QY	6241	GAACCTGTAAAGTGAAGCGCCGCCACATTCGGGCAGATCTAAATTTGGCTATGGGGCAAG	6300
Db	6241	GAACCTGTAAAGTGAAGCGCCGCCACATTCGGGCAGATCTAAATTTGGCTATGGGGCAAG	6300
QY	6301	GACGTCCGGAACTATCCAGCAAGGCGCTTAACACATCCGCTCCGTGTGAAGGACTTG	6360
Db	6301	GACGTCCGGAACTATCCAGCAAGGCGCTTAACACATCCGCTCCGTGTGAAGGACTTG	6360
QY	6361	CTGGAAGACACTGAGACACCAATTGACACCACTATGCAAAAATAGAGTTTTCGC	6420
Db	6361	CTGGAAGACACTGAGACACCAATTGACACCACTATGCAAAAATAGAGTTTTCGC	6420
QY	6421	GTCCAACCCAGAAAGGGGGGCGCAAGCCAGCTCCGCTTATGTATTCOCAGATTTGGG	6480
Db	6421	GTCCAACCCAGAAAGGGGGGCGCAAGCCAGCTCCGCTTATGTATTCOCAGATTTGGG	6480
QY	6481	GTTGCTGTATGACGAAGAAATGAGCCCTTATACGATGTGTTCCACCCTCCCTAGGCGCTG	6540
Db	6481	GTTGCTGTATGACGAAGAAATGAGCCCTTATACGATGTGTTCCACCCTCCCTAGGCGCTG	6540
QY	6541	ATGGGCTCTTCATACGATTCCAATACTCTCTCGACACCGGGGTGAGTTCTCGTGAAT	6600
Db	6541	ATGGGCTCTTCATACGATTCCAATACTCTCTCGACACCGGGGTGAGTTCTCGTGAAT	6600
QY	6601	GCTCGGAAGCGAAGAAATCCCTATAGGGCTTGCGATATGACACCGCGTATTGACGA	6660
Db	6601	GCTCGGAAGCGAAGAAATCCCTATAGGGCTTGCGATATGACACCGCGTATTGACGA	6660
QY	6661	ACGGTCACTGAGATGACATTCGCTGTTGAGAGATCAATACCATTGTTGACTTGGC	6720
Db	6661	ACGGTCACTGAGATGACATTCGCTGTTGAGAGATCAATACCATTGTTGACTTGGC	6720
QY	6721	CCCGAAGCCACAGCGCCATTAAGTGTGCTGACAGACGCGCTTACATCGGGGGCCCCCTG	6780
Db	6721	CCCGAAGCCACAGCGCCATTAAGTGTGCTGACAGACGCGCTTACATCGGGGGCCCCCTG	6780
QY	6781	ACTAATTCTAAAGGGCGAGACTGGGCTATCGCGGCTGCGGCGAGGGGTACTGAGC	6840
Db	6781	ACTAATTCTAAAGGGCGAGACTGGGCTATCGCGGCTGCGGCGAGGGGTACTGAGC	6840
QY	6841	ACCAAGCTGGTAAATACCTTCACATGTTACTTGAAGCGCGCTGCGGCTGTGAGACTCG	6900
Db	6841	ACCAAGCTGGTAAATACCTTCACATGTTACTTGAAGCGCGCTGCGGCTGTGAGACTCG	6900
QY	6901	AAGCTCCAGGACTGACAGATGCTCGATGATGGGAGAGACCTTGTTATCTGTGAAGC	6960
Db	6901	AAGCTCCAGGACTGACAGATGCTCGATGATGGGAGAGACCTTGTTATCTGTGAAGC	6960
QY	6961	CGCGGAGCCCAAGAGAGAGCGGAGCTTACGAGGCCCTTCAGGAGCTATGACTAGATAC	7020

Db	6961	GGGGGGACCCAAAGAGACAGAGGGGACCCTTACGGGCTTACAGAGGCTATGACTAGATAC	7020
QY	7021	TCCTGCCCCCTGGGGACCCGCCAAACAGAAATACGACTTGGAGTTATATACATCATGC	7080
Db	7021	TCCTGCCCCCTGGGGACCCGCCAAACAGAAATACGACTTGGAGTTATATACATCATGC	7080
QY	7081	TCCTCCATGTTGTTAGTCGGGACAGATGCATCTGGCAAAAGGGTTACTATCTACCCGT	7140
Db	7081	TCCTCCATGTTGTTAGTCGGGACAGATGCATCTGGCAAAAGGGTTACTATCTACCCGT	7140
QY	7141	GACCCACACACCCCCCTTGGGGGGGCTGGGTGGGAGACAGCTAGACACACTCCAGTCAT	7200
Db	7141	GACCCACACACCCCCCTTGGGGGGGCTGGGTGGGAGACAGCTAGACACACTCCAGTCAT	7200
QY	7201	TCCTGGCTAGGCAACATCATCATGATATAGGGCCACCCTTGTGGCAAGATGATCCTGATG	7260
Db	7201	TCCTGGCTAGGCAACATCATCATGATATAGGGCCACCCTTGTGGCAAGATGATCCTGATG	7260
QY	7261	ACCTATTTCTCTCCATCCTCTTCAAGTCAGAGAACACTTGAAAAAGCCCTAATTTGTAG	7320
Db	7261	ACCTATTTCTCTCCATCCTCTTCAAGTCAGAGAACACTTGAAAAAGCCCTAATTTGTAG	7320
QY	7321	ATCTACGGGGCTGTGTACTCCATTGAGGCCATTGACCTACCTCAATCATTCACGACTC	7380
Db	7321	ATCTACGGGGCTGTGTACTCCATTGAGGCCATTGACCTACCTCAATCATTCACGACTC	7380
QY	7381	CATGGCCCTTACGGCATTTTCACTCACTCAATGACTCTCCAGGAGAGATCAATAGGGTGGCT	7440
Db	7381	CATGGCCCTTACGGCATTTTCACTCACTCAATGACTCTCCAGGAGAGATCAATAGGGTGGCT	7440
QY	7441	TCATGCTCAGAGAACTTGGGGATACGGCCCTTGGAGTCTGGAGACATCGGGCCAGAGT	7500
Db	7441	TCATGCTCAGAGAACTTGGGGATACGGCCCTTGGAGTCTGGAGACATCGGGCCAGAGT	7500
QY	7501	GTCGGCGCTTAGGCTACTGTCTCCAGGGGGGAGGGGCTGCACATTGTGGCAAGTACCTCTTC	7560
Db	7501	GTCGGCGCTTAGGCTACTGTCTCCAGGGGGGAGGGGCTGCACATTGTGGCAAGTACCTCTTC	7560
QY	7561	AACCTGGCAGTAGAGGCCAACACTGAACTCACTCCATCCCGGCTGCGTCCACGTTGAT	7620
Db	7561	AACCTGGCAGTAGAGGCCAACACTGAACTCACTCCATCCCGGCTGCGTCCACGTTGAT	7620
QY	7621	TTATCCACACTGCTGCTGTGTGTAGAGGGGGGAGACATATATCACAGCCTCTCTGT	7680
Db	7621	TTATCCACACTGCTGCTGTGTGTAGAGGGGGGAGACATATATCACAGCCTCTCTGT	7680
QY	7681	GCCCGACCCCGCTGTTCACTGCTGTGCTCACTCTCTTCTGTAGGGGTAGGCATCTAT	7740
Db	7681	GCCCGACCCCGCTGTTCACTGCTGTGCTCACTCTCTTCTGTAGGGGTAGGCATCTAT	7740
QY	7741	CTACACCCCAACCCATATACGGGGAGTAAACACTCCACAGCCCAATAGGCCATCCGTTT	7800
Db	7741	CTACACCCCAACCCATATACGGGGAGTAAACACTCCACAGCCCAATAGGCCATCCGTTT	7800
QY	7801	TTTCCCTTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
Db	7801	TTTCCCTTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7860
QY	7861	TTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
Db	7861	TTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	7920
QY	7921	TAGCGTAAAGGTCCTGTAGCGGCTGATGTAGAGAGAGGCTGATACGAGGCTCTGTC	7980
Db	7921	TAGCGTAAAGGTCCTGTAGCGGCTGATGTAGAGAGAGGCTGATACGAGGCTCTGTC	7980
QY	7981	AGATCAAGT 7989	
Db	7981	AGATCAAGT 7989	

RESULT 10

AAD25321
ID AAD25321 standard; cDNA; 7987 BP.
XX
AC AAD25321;
XX
DT 12-MAR-2002 (first entry)
XX
DE Hepatitis C virus (HCV) replBartman/delta20's cDNA.
XX
KM Hepatitis C virus; HCV, transfection; infection; virus neutralisation;
KM gene therapy; vaccine; immunoprotection; hepatotropic; virulence; liver;
KM ss.
XX
OS Hepatitis C virus.
XX
PN MO200189364-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001MO-US16822.
XX
PR 23-MAY-2000; 2000US-0576989.
XX
PA (UNIM) UNIV WASHINGTON.
XX
PI Rice CM, Blight KJ;
XX
DR WPI; 2002-066755/09.
XX
PT Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences
PT
XX
PS Claim 44; Page 66-69; 174pp; English.
XX
CC The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop in vitro and in vivo assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets,
CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficient replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays,
CC production of immunogenic HCV particles for vaccination, engineering of
CC attenuated HCV derivatives as possible vaccine candidates, engineering
CC of attenuated or defective HCV derivatives for expression of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) replBartman/delta20's cDNA.
XX
SQ Sequence 7987 BP; 1647 A; 2368 C; 2243 G; 1729 T; 0 other;

Query Match 99.7%; Score 7968.6; DB 24; Length 7987;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7983; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 1 GCCAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAAGTACTG 60
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DB 1 GCCAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAAGTACTG 60
QY 1 TCTTCAGCGAAGAGCGCTTAGCCATGGCTTAGTATGATGCTGTGGAGCCCTCCAGGAC 120
61 TCTTCAGCGAAGAGCGCTTAGCCATGGCTTAGTATGATGCTGTGGAGCCCTCCAGGAC 120
DB 61 TCTTCAGCGAAGAGCGCTTAGCCATGGCTTAGTATGATGCTGTGGAGCCCTCCAGGAC 120
QY 121 CCCCCCTCCCGGGAGAGCCATAGTGTCTCTCGAGAACCGGTGAGTACACCGGAATTCGCG 180
121 CCCCCCTCCCGGGAGAGCCATAGTGTCTCTCGAGAACCGGTGAGTACACCGGAATTCGCG 180
DB 121 CCCCCCTCCCGGGAGAGCCATAGTGTCTCTCGAGAACCGGTGAGTACACCGGAATTCGCG 180
QY 181 GACGACCGGCTCTTCTTCTGATTAACCCGCTCAATGCCCTGGAGATTGGGCGTCCGCC 240
181 GACGACCGGCTCTTCTTCTGATTAACCCGCTCAATGCCCTGGAGATTGGGCGTCCGCC 240
DB 181 GACGACCGGCTCTTCTTCTGATTAACCCGCTCAATGCCCTGGAGATTGGGCGTCCGCC 240
QY 241 GCGAGACTGTAGCGCGATAGTGTGGGTGCGGAAGCGCTTGTGATGCTGCTGATAG 300
241 GCGAGACTGTAGCGCGATAGTGTGGGTGCGGAAGCGCTTGTGATGCTGCTGATAG 300
DB 241 GCGAGACTGTAGCGCGATAGTGTGGGTGCGGAAGCGCTTGTGATGCTGCTGATAG 300
QY 301 GTGCTTGGAGTGGCCCGGGAGGCTCTGTAGACCGGTGACACATGAGCAGCAATCTTAAC 360
301 GTGCTTGGAGTGGCCCGGGAGGCTCTGTAGACCGGTGACACATGAGCAGCAATCTTAAC 360
DB 301 GTGCTTGGAGTGGCCCGGGAGGCTCTGTAGACCGGTGACACATGAGCAGCAATCTTAAC 360
QY 361 CTCAGAGAAACCAAGAGGGCGCCCATGATGACAGAGATGGATTGACAGCAGGTTCTC 420
361 CTCAGAGAAACCAAGAGGGCGCCCATGATGACAGAGATGGATTGACAGCAGGTTCTC 420
DB 361 CTCAGAGAAACCAAGAGGGCGCCCATGATGACAGAGATGGATTGACAGCAGGTTCTC 420
QY 421 CGGCGGCTTGGGTGAGAGGCTATTGGGCTATGACTGGGCAACAACAGACATCGCTGCT 480
421 CGGCGGCTTGGGTGAGAGGCTATTGGGCTATGACTGGGCAACAACAGACATCGCTGCT 480
DB 421 CGGCGGCTTGGGTGAGAGGCTATTGGGCTATGACTGGGCAACAACAGACATCGCTGCT 480
QY 481 CTGATGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
481 CTGATGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 CTGATGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 ACCTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
541 ACCTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 ACCTGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CGAGGCGGCTTCTTGGGCGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
601 CGAGGCGGCTTCTTGGGCGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 CGAGGCGGCTTCTTGGGCGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 TGTATTGGGCGAAGTGGCGGGGCGAGGATCTCTGTATCTCACTGCTGCTGCTGCTGCT 720
661 TGTATTGGGCGAAGTGGCGGGGCGAGGATCTCTGTATCTCACTGCTGCTGCTGCTGCT 720
DB 661 TGTATTGGGCGAAGTGGCGGGGCGAGGATCTCTGTATCTCACTGCTGCTGCTGCTGCT 720
QY 721 AAGTATCCATATGCTGCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
721 AAGTATCCATATGCTGCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 AAGTATCCATATGCTGCTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CATTGACACCAAGCGAAGCAATGCAATGCAAGCGAGCAGCTACTGATGGAACCGGTC 840
781 CATTGACACCAAGCGAAGCAATGCAATGCAAGCGAGCAGCTACTGATGGAACCGGTC 840
DB 781 CATTGACACCAAGCGAAGCAATGCAATGCAAGCGAGCAGCTACTGATGGAACCGGTC 840
QY 841 TTGTGATCAGATGATGTGTGACAGCAAGCATGAGGGGCTGCGGCCCGCAACTGTTCG 900
841 TTGTGATCAGATGATGTGTGACAGCAAGCATGAGGGGCTGCGGCCCGCAACTGTTCG 900
DB 841 TTGTGATCAGATGATGTGTGACAGCAAGCATGAGGGGCTGCGGCCCGCAACTGTTCG 900
QY 901 CCAGGCTAAGGCGCGATGCTGCGCGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
901 CCAGGCTAAGGCGCGATGCTGCGCGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 CCAGGCTAAGGCGCGATGCTGCGCGAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GCTTCCGGAATATCATGTGTGAAAAATGCGCCCTTTCTGATTTATGACTGTGGCGGCG 1020
961 GCTTCCGGAATATCATGTGTGAAAAATGCGCCCTTTCTGATTTATGACTGTGGCGGCG 1020
DB 961 GCTTCCGGAATATCATGTGTGAAAAATGCGCCCTTTCTGATTTATGACTGTGGCGGCG 1020
QY 1021 TGGGCTGCGGACCGCTATGAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1021 TGGGCTGCGGACCGCTATGAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 TGGGCTGCGGACCGCTATGAGGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 TTGGCGGCGAATGAGGCTATCGGCTTCTGCTGCTTAAAGGATGCGCGCTCCGATTGCG 1140
1081 TTGGCGGCGAATGAGGCTATCGGCTTCTGCTGCTTAAAGGATGCGCGCTCCGATTGCG 1140
DB 1081 TTGGCGGCGAATGAGGCTATCGGCTTCTGCTGCTTAAAGGATGCGCGCTCCGATTGCG 1140

QY 1141 AGGCGATGCGCTTCTATCGCCCTTCTGACGAGTCTTCTGAGTTAAACAGCACAAACG 1200
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Db 1141 AGGCGATGCGCTTCTATCGCCCTTCTGACGAGTCTTCTGAGTTAAACAGCACAAACG 1200
QY 1201 GTTCCCTTAGCGGGGATCAATCGGCCCTCTCCCTCCCGCCCCCTTAAGCTTACTGGC 1260
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Db 1201 GTTCCCTTAGCGGGGATCAATCGGCCCTCTCCCTCCCGCCCCCTTAAGCTTACTGGC 1260
QY 1261 CGAAGCGGCTTGAATTAAGCGCGGTGTGCGTTTGTCTATATGTATTTTCCACCATATTG 1320
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Db 1261 CGAAGCGGCTTGAATTAAGCGCGGTGTGCGTTTGTCTATATGTATTTTCCACCATATTG 1320
QY 1321 CCGTCTTTTGGCAATGTGAGGGCGCCGGAACCTGGCCCTGTCTTCTTAAGCAGCATTTCT 1380
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Db 1321 CCGTCTTTTGGCAATGTGAGGGCGCCGGAACCTGGCCCTGTCTTCTTAAGCAGCATTTCT 1380
QY 1381 AGGGGCTCTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGATATGTGTGAGGAAGCA 1440
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Db 1381 AGGGGCTCTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGATATGTGTGAGGAAGCA 1440
QY 1441 GTTCCCTTGAAGCTTCTTGAAGACAAACGCTGTGAGCAGCCCTTTCAGCGACGG 1500
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Db 1441 GTTCCCTTGAAGCTTCTTGAAGACAAACGCTGTGAGCAGCCCTTTCAGCGACGG 1500
QY 1501 AACCCCGCACTGGCGACAGTGGCTCTGCGCCAAAGCCAGCTGTATAGATACACT 1560
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Db 1501 AACCCCGCACTGGCGACAGTGGCTCTGCGCCAAAGCCAGCTGTATAGATACACT 1560
QY 1561 GCAAGCGGGACACACCCAGTGCACGTTGTGAGTTGAGTATGTTGGAAGAGTCAA 1620
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Db 1561 GCAAGCGGGACACACCCAGTGCACGTTGTGAGTTGAGTATGTTGGAAGAGTCAA 1620
QY 1621 TGCTCTCCGCAAGCTATTCAACAAAGGGGCTGAGGATGCCCCAAGATGCCCATTTGT 1680
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Db 1621 TGCTCTCCGCAAGCTATTCAACAAAGGGGCTGAGGATGCCCCAAGATGCCCATTTGT 1680
QY 1681 ATGGATCTGATCTGGGGGCTCGGTGCACATGCTTTACATGTTTACTGAGGTAA 1740
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Db 1681 ATGGATCTGATCTGGGGGCTCGGTGCACATGCTTTACATGTTTACTGAGGTAA 1740
QY 1741 AACGTAGGCCCCCGGACACAGGGGAGTGGTTTCTTGAAGAAACAGATATACC 1800
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Db 1741 AACGTAGGCCCCCGGACACAGGGGAGTGGTTTCTTGAAGAAACAGATATACC 1800
QY 1801 ATGGCGCTATTAGGCGCTACTCCACACAGAGCGAGGCTACTTGGCTGCATCATCT 1860
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Db 1801 ATGGCGCTATTAGGCGCTACTCCACACAGAGCGAGGCTACTTGGCTGCATCATCT 1860
QY 1861 AGCTCTACAGGGCGGAGCAAGCAAGTCCAGGGGAGGTCCAGGTGTCTCCACGGCA 1920
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Db 1861 AGCTCTACAGGGCGGAGCAAGCAAGTCCAGGGGAGGTCCAGGTGTCTCCACGGCA 1920
QY 1921 ACACAATCTTCTGCGACCTGCGTCAATGCGGTGTGTGAGTGTCTATCATGTGCC 1980
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Db 1921 ACACAATCTTCTGCGACCTGCGTCAATGCGGTGTGTGAGTGTCTATCATGTGCC 1980
QY 1981 GGCTCAAGACCCCTTCCGCGCCCAAGGGCCCAATCACCCAAATGTACCAATGTGAC 2040
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Db 1981 GGCTCAAGACCCCTTCCGCGCCCAAGGGCCCAATCACCCAAATGTACCAATGTGAC 2040
QY 2041 CAGGACCTGTGGGTGAGCAAGCGCCCGGGGGGCGTCTTCTTGAACCACTGACCTGC 2100
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Db 2041 CAGGACCTGTGGGTGAGCAAGCGCCCGGGGGGCGTCTTCTTGAACCACTGACCTGC 2100
QY 2101 GGGAGTCTGGACCTTACTTGTGTACGAGGCAATGCGATGTCCGCTGCGCGCGG 2160
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Db 2101 GGGAGTCTGGACCTTACTTGTGTACGAGGCAATGCGATGTCCGCTGCGCGCGG 2160
QY 2161 GGGGACAGGAGGGAGGCTACTTCCCGCAGCGCCGCTCTCTACTTGAAGGGCTTTGC 2220
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Db 2161 GGGGACAGGAGGGAGGCTACTTCCCGCAGCGCCGCTCTCTACTTGAAGGGCTTTGC 2220

QY 2221 GGGGTCACACTGCTTGTCCCTCGGGGACAGCTGTGGGCATCTTTCGGGCTGCCGTGC 2280
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Db 2221 GGGGTCACACTGCTTGTCCCTCGGGGACAGCTGTGGGCATCTTTCGGGCTGCCGTGC 2280
QY 2281 ACCCGAGGGGTTCGGAAGCGGTGACTTTGTACCCCGTGAAGTCTATGGAACCACTATG 2340
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Db 2281 ACCCGAGGGGTTCGGAAGCGGTGACTTTGTACCCCGTGAAGTCTATGGAACCACTATG 2340
QY 2341 CGTCCCGGATCTTACGAGCAACTGTCCTCCCGCGGCGTACCGCAGACATTCAGGTG 2400
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Db 2341 CGTCCCGGATCTTACGAGCAACTGTCCTCCCGCGGCGTACCGCAGACATTCAGGTG 2400
QY 2401 GCCCATCTACGCGCCCTTACTGTGTAGCGGCAAGACACTAAGTTCGCGGTATGCA 2460
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Db 2401 GCCCATCTACGCGCCCTTACTGTGTAGCGGCAAGACACTAAGTTCGCGGTATGCA 2460
QY 2461 GCCAAGGGATTAAGTGTCTTGTGTAACCGGTGCGCGGCGACCTAGTGTGGG 2520
|||||
Db 2461 GCCAAGGGATTAAGTGTCTTGTGTAACCGGTGCGCGGCGACCTAGTGTGGG 2520
QY 2521 GCGTATATGTCTAAGGCACATGATCGACCCCTAATCAGAACCGGGGTAAAGCACATC 2580
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Db 2521 GCGTATATGTCTAAGGCACATGATCGACCCCTAATCAGAACCGGGGTAAAGCACATC 2580
QY 2581 ACCAGGGGTGCCCCCATCAGTACTCCACTATGGCAGTTTCTTCCGAGGGTGTGC 2640
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Db 2581 ACCAGGGGTGCCCCCATCAGTACTCCACTATGGCAGTTTCTTCCGAGGGTGTGC 2640
QY 2641 TCTGGGGGGCCTATGACATCATATATGTATGATGATGCCACTGACTCCAGCACT 2700
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Db 2641 TCTGGGGGGCCTATGACATCATATATGTATGATGATGCCACTGACTCCAGCACT 2700
QY 2701 ATCTGGGATGGGACACATCTCTGACCAAGGGGAGAGCGGTGAGCGGCATCTGTGTG 2760
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Db 2701 ATCTGGGATGGGACACATCTCTGACCAAGGGGAGAGCGGTGAGCGGCATCTGTGTG 2760
QY 2761 CTGGCCACCGCTACGCTCCGGGATCGGATCGACCGGACATCCCAACATGAGAGGTG 2820
|||||
Db 2761 CTGGCCACCGCTACGCTCCGGGATCGGATCGACCGGACATCCCAACATGAGAGGTG 2820
QY 2821 GCTGTGTCCAGACTGGAGAAATCCCTTTTATGGCAAGCGATCCCATCGAGACATC 2880
|||||
Db 2821 GCTGTGTCCAGACTGGAGAAATCCCTTTTATGGCAAGCGATCCCATCGAGACATC 2880
QY 2881 AAGGGGGGAGGACCTATTTTCTGCCATTCCAAAGAAATGTGATGAGCTGGCGCG 2940
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Db 2881 AAGGGGGGAGGACCTATTTTCTGCCATTCCAAAGAAATGTGATGAGCTGGCGCG 2940
QY 2941 AAGCTGTCCGCTCGGACTCAATGCTGTAGCATATTCGCGGCTTTGATGTATCCGTC 3000
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Db 2941 AAGCTGTCCGCTCGGACTCAATGCTGTAGCATATTCGCGGCTTTGATGTATCCGTC 3000
QY 3001 ATACCACTAGGAGGAGAGCTATTTGCTAGCAAGCGGCTTAATAGCAGGGCTTACC 3060
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Db 3001 ATACCACTAGGAGGAGAGCTATTTGCTAGCAAGCGGCTTAATAGCAGGGCTTACC 3060
QY 3061 GGGGATTTGACTCATGTATGACTGCATATCATGTGTACCCAGACAGTGTAGCTTACC 3120
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Db 3061 GGGGATTTGACTCATGTATGACTGCATATCATGTGTGTACCCAGACAGTGTAGCTTACC 3120
QY 3121 CTGGACCGGACCTTCAACATGTAGAGCAGACGCGGCGACAGAGCGGGTGTACGCTGC 3180
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Db 3121 CTGGACCGGACCTTCAACATGTAGAGCAGACGCGGTGTACGAGCGGGTGTACGCTGC 3180
QY 3181 CAGCGCCAGGACAGACTGTAGGGGAGATGGGCAATTAACAGTTGTGACTCCAGA 3240
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Db 3181 CAGCGCCAGGACAGACTGTAGGGGAGATGGGCAATTAACAGTTGTGACTCCAGA 3240
QY 3241 GAAAGCGCCTCGGGCATTTGATTCCTGCGGTGTGTGCGAGTGTGTGACGCGGGCTGT 3300
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Db 3241 GAAAGCGCCTCGGGCATTTGATTCCTGCGGTGTGTGCGAGTGTGTGACGCGGGCTGT 3300
QY 3301 GCTTGTAGAGACTACGCGCGGAGACCTCACTTGAAGTTGCGGGCTTACTTAACACA 3360
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Db 3301 GCTTGGTAGAGCTACACCCGCGAGACCTAGTGAAGTTGCGGGCTTACTTAAACA 3360
Qy 3361 CCAGGGTTGCCGTCCTGCCAGAGACATGTGAGTTCTGGAGAGCGTCTTACAGCGCTC 3420
Db 3361 CCAGGGTTGCCGTCCTGCCAGAGACATGTGAGTTCTGGAGAGCGTCTTACAGCGCTC 3420
Qy 3421 ACCACATAGAGCGCCATTCTTGTCCAGACTAAGAGGAGAGACAATCCCTAC 3480
Db 3421 ACCACATAGAGCGCCATTCTTGTCCAGACTAAGAGGAGAGACAATCCCTAC 3480
Qy 3481 CTGTAGACATACAGGCTACAGGTGTGCGCAGGCGCTCAGGCTCCACTCCATGCTGGAC 3540
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Db 3781 ATCATCTGTGCGGAAGCGCGCCATCATTTCCGACAGGGAAGTCCCTTACCGGAGTTC 3840
Qy 3841 GATGAGATGSAAGAGTGGGCTCACACTCCCTACATGCAACAGGGAATGAGCTGCC 3900
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Db 4021 TGGAAATTCATCAGCGGATACATATTATAGACAGCTTGCACACTGCTGGCAACCC 4080
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Db 4081 GCGATAGATCAGTGAATGAGCTTACAGACCTTATCCAGCCCGCTCACACCAACAT 4140
Qy 4141 ACCCTCGTGTAAACATCTCTGGGGAGTGGTGGCGCCCAACCTGTGCTCCAGCGCT 4200
Db 4141 ACCCTCGTGTAAACATCTCTGGGGAGTGGTGGCGCCCAACCTGTGCTCCAGCGCT 4200
Qy 4201 GCTTCTGCTTTCGTAGGCGCGGATGCTGAGAGCGGCTTGGCAACATAGGCTTGG 4260
Db 4201 GCTTCTGCTTTCGTAGGCGCGGATGCTGAGAGCGGCTTGGCAACATAGGCTTGG 4260
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Db 4261 AAGGTGCTGTGATATTGAGGAGTTATGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 4320
Qy 4321 TTTAAGTATGAGAGGAGAGATGCTCCACGAGAGAGGAGGAGGAGGAGGAGGAGG 4380
Db 4321 TTTAAGTATGAGAGGAGAGATGCTCCACGAGAGAGGAGGAGGAGGAGGAGGAGG 4380
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Qy 4621 GAGGAGCTCCACAGCAGTCTGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4680
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Db 4801 CAACACACCTCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4860
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Db 4921 ACCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4980
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Db 4981 GCTGCTGAGAGTACGTGAGGAGTACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5040
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Db 5101 GATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5160
Qy 5161 ACATTCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5220
Db 5161 ACATTCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5220
Qy 5221 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5280
Db 5221 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5280
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Db 5281 GCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5340
Qy 5341 CTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5400
Db 5341 CTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5400
Qy 5401 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5460
Db 5401 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5460
Qy 5461 TCGAATAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5520
Db 5461 TCGAATAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5520

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QY 5521 AGGAGATATCCGTTCCGGCGGAGATCTGCGGAGGTTCCAGAAATTCCTCCGAGCGATG 5580
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Db 5521 AGGAAATATCCGTTCCGGCGGAGATCTGCGGAGGTTCCAGAAATTCCTCCGAGCGATG 5580
QY 5581 CCCATATGCGACGCCCGGATTTACAACCCCTGTAAGTCTGGAAGACCCGGAC 5640
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Db 5581 CCCATATGCGACGCCCGGATTTACAACCCCTGTAAGTCTGGAAGACCCGGAC 5640
QY 5641 TACGTCCCTCAAGTGTACACGGGTGTCATGCGCCCTGCAAGGCCCTCCGATACCA 5700
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Db 5641 TACGTCCCTCAAGTGTACACGGGTGTCATGCGCCCTGCAAGGCCCTCCGATACCA 5700
QY 5701 CTTCCACGAGAGAAAGAGCGTTGTCTGTGCAAAATCTACCGTGTCTCTCTGCGG 5760
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Db 5701 CTTCCACGAGAGAAAGAGCGTTGTCTGTGCAAAATCTACCGTGTCTCTCTGCGG 5760
QY 5761 GAGCTGCGCAAAAGACCTTCGCGACCTCCGAATGCTGGCCGTGACACGCGCACGGCA 5820
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Db 5761 GAGCTGCGCAAAAGACCTTCGCGACCTCCGAATGCTGGCCGTGACACGCGCACGGCA 5820
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QY 5881 TCCCTCCATGCCCCCTTGAAGGGGAGCCGGGGGATCCCGATCTCAGGACGGTCTTGG 5940
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Db 5941 TCTACCGTAAGCGAGAGGCTAGTGAAGAGCTGCTGCTGCTGATGCTCTACACATGG 6000
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Db 6121 CTGGGGGAGAGAGGTCACCTTGAACACTGACAGTCCGAGTCCGAGACCACTACCGGGAC 6180
QY 6181 GTGCTCAAGSAGATGAAGGGAAGGCGTCCACAGTTAAGGCTAACTTCTATCCGTGAG 6240
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Db 6181 GTGCTCAAGSAGATGAAGGGAAGGCGTCCACAGTTAAGGCTAACTTCTATCCGTGAG 6240
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Db 6301 GAGCTCGGAACCTATCCAGCAAGGCCGTTAAACCAATCCGCTCGGTGGAAGACTG 6360
QY 6361 CTGAGAGACCTGAGACACCAATTGACACCCACCATATGCAAAAATGAGGTTTTCTGC 6420
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Db 6361 CTGAGAGACCTGAGACACCAATTGACACCCACCATATGCAAAAATGAGGTTTTCTGC 6420
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Db 6421 GTCCCAACAGAGAAAGGGGGGCGCAAGCCAGCTCGGCTATGCTATGCCAGATTGGG 6480
QY 6481 GTTCGTGTGTGCGAGAAAATGGCCTTTAGATGTGTGTCTCCACCCTCCCTCAGGCGTG 6540
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Db 6481 GTTCGTGTGTGCGAGAAAATGGCCTTTAGATGTGTGTCTCCACCCTCCCTCAGGCGTG 6540
QY 6541 ATGGGCTCTTCATAGGATTTCCAAATCTCTCTGAGACAGCGGCTGAGTCTCTGTGAT 6600
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Db 6541 ATGGGCTCTTCATAGGATTTCCAAATCTCTCTGAGACAGCGGCTGAGTCTCTGTGAT 6600
QY 6601 GCCTGGAAAGCAGAGAAATGCCCTATGSGCTTCGATATGACACCCGCTTTGACTCA 6660
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Db 6601 GCCTGGAAAGCAGAGAAATGCCCTATGSGCTTCGATATGACACCCGCTTTGACTCA 6660
QY 6661 ACGGTACTAGAGATGACATCCGTTGAGAGAGTCAATCTACCAATGTTGTGACTGGCC 6720
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Db 6661 ACGGTACTAGAGATGACATCCGTTGAGAGAGTCAATCTACCAATGTTGTGACTGGCC 6720
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QY 6781 ACTAATTTCTAAAGGCGAGACTGCGGCTATGCGCGGTGCGCGGAGCGGTGTACTAGC 6840
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Db 6781 ACTAATTTCTAAAGGCGAGACTGCGGCTATGCGCGGTGCGCGGAGCGGTGTACTAGC 6840
QY 6841 ACCAGCTGCGGTATACCTTCACATGTTACTTGAAGCGCGCTGCGGCTGTGAGACTGC 6900
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QY 6901 AAGCTCCAGAGACTGACAGATGCTGATGCGAGACGACCTTGTGTTATCTGTAAGC 6960
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Db 6901 AAGCTCCAGAGACTGACAGATGCTGATGCGAGACGACCTTGTGTTATCTGTAAGC 6960
QY 6961 GCGGGACCCCAAGACAGAGAGCGGAGCTTACGCGCTTACAGGAGCTATGACTAGATAC 7020
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QY 7021 TCTGCCCCCTGSGGAGCCGCCCAACAGAAATACGACTTGAATGATTAACATCAGC 7080
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Db 7021 TCTGCCCCCTGSGGAGCCGCCCAACAGAAATACGACTTGAATGATTAACATCAGC 7080
QY 7081 TCTCTCAATGTGTCAATGCTGCGACGATGCTATGCGAAAAGGTTACTATCTACCCGT 7140
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Db 7081 TCTCTCAATGTGTCAATGCTGCGACGATGCTATGCGAAAAGGTTACTATCTACCCGT 7140
QY 7141 GACCCCAACACCCCTTGGCGGGGCTGCGTGGAGACAGCTAGACACCTCCAGTCAAT 7200
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Db 7141 GACCCCAACACCCCTTGGCGGGGCTGCGTGGAGACAGCTAGACACCTCCAGTCAAT 7200
QY 7201 TCTGTGCTAGGACACATCATATGATGAGTCCGACCTTGTGGCAAGATATCCTGATG 7260
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Db 7201 TCTGTGCTAGGACACATCATATGATGAGTCCGACCTTGTGGCAAGATATCCTGATG 7260
QY 7261 ACTCATTTTCTTCCATCCCTTCTAGTCAAGSACAATGAAAGGCCCTGATTTGATG 7320
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Db 7261 ACTCATTTTCTTCCATCCCTTCTAGTCAAGSACAATGAAAGGCCCTGATTTGATG 7320
QY 7321 ATCTAGGGGCGCTGTACTTCATTTGAGCCACTTGAACCTACATCATCAAGSACTC 7380
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Db 7321 ATCTAGGGGCGCTGTACTTCATTTGAGCCACTTGAACCTACATCATCAAGSACTC 7380
QY 7381 CATGGGCTTAGGCACTTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGGTTGCT 7440
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Db 7381 CATGGGCTTAGGCACTTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGGTTGCT 7440
QY 7441 TCAATGCTTAGGAACTTGGGATACCGGCTTGGAGTCTGAGACATCGGCGCAAGAT 7500
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Db 7441 TCAATGCTTAGGAACTTGGGATACCGGCTTGGAGTCTGAGACATCGGCGCAAGAT 7500
QY 7501 GTCCGGCTAGGCTACTGTCCAGGAGGAGGAGGTGTCACCTGAGGCAATTAAGTCTGTC 7560
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Db 7501 GTCCGGCTAGGCTACTGTCCAGGAGGAGGAGGTGTCACCTGAGGCAATTAAGTCTGTC 7560
QY 7561 AACTGGGCAATGAAGCAAGCTCAAACTCACTCCATCCGCGTCCGCTCCAGTTGAT 7620
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Db 7561 AACTGGGCAATGAAGCAAGCTCAAACTCACTCCATCCGCGTCCGCTCCAGTTGAT 7620
QY 7621 TTAATCAGGCTGTGTTCTGTTACAGCGGGGAGACATATATCAAGCTGTGCTGCT 7680
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Db 7621 TTAATCAGGCTGTGTTCTGTTACAGCGGGGAGACATATATCAAGCTGTGCTGCT 7680
QY 7681 GCCGAGCCCGGCTGTTCTATGTGTGCTACTCTACTTCTGTAGGGGTAGGCATCTAT 7740
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Db 7661 GCCCGACCCCGGTCGTCAGTGTGCTACTCTACTTCTGTAGGGTAGGACATCAT 7740
Qy 7741 CTACTCCCAACCGATGAGGGAGGTAAACACTCCAGGCCATAGGCCATCTGTTT 7800
Db 7741 CTACTCCCAACCGATGAGGGAGGTAAACACTCCAGGCCATAGGCCATCTGTTT 7800
Qy 7801 TTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
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Qy 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7869 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7918
Qy 7921 TAGCTGTAAAGTCCGTGAGCCGCTTGACTGCAGAGAGTGTGATAGCTGCTCTGTC 7980
Db 7919 TAGCTGTAAAGTCCGTGAGCCGCTTGACTGCAGAGAGTGTGATAGCTGCTCTGTC 7978
Qy 7981 AGATCAGT 7989
Db 7979 AGATCAGT 7987

RESULT 11
AAD25329
ID AAD25329 standard; cDNA; 7987 BP.
XX
AC AAD25329;
XX
DT 12-MAR-2002 (first entry)
XX
DE Hepatitis C virus (HCV) adaptive replicon VII cDNA.
XX
KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
KW gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
KW adaptive replicon VII; ss.
XX
OS Hepatitis C virus.
XX
PN WO200189364-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US16822.
XX
PR 23-MAY-2000; 2000US-0576989.
XX
PA (UNIT) UNIV WASHINGTON.
XX
PI Rice CM, Blight KJ;
XX
DR WPI; 2002-066755/09.
XX
PT Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences
PT
XX
PS Disclosure; Page 84-87; 174pp; English.
XX
CC The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop in vitro and in vivo assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets.

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CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficiency replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays.
CC production of immunogenic HCV particles for vaccination assays.
CC attenuation of HCV derivatives as possible vaccine candidates, engineering
CC of attenuated or defective HCV derivatives for expression of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) adaptive replicon VII cDNA.
XX
SO Sequence 7987 BP; 1647 A; 2368 C; 2242 G; 1730 T; 0 other;

Query Match 99.7%; Score 7967; DB 24; Length 7987;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7982; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy 1 GCCAGCCCCGATTTGGGGGAGACACTCCACATAGTCACTCCCTGTAGGAATCTAG 60
Db 1 GCCAGCCCCGATTTGGGGGAGACACTCCACATAGTCACTCCCTGTAGGAATCTAG 60
Qy 61 TCTTACAGCAGAAAGCGTCTAGCCATGGCTTAGTATGATGATGATGATGATGATGAT 120
Db 61 TCTTACAGCAGAAAGCGTCTAGCCATGGCTTAGTATGATGATGATGATGATGATGAT 120
Qy 121 CCCCCCTCCCGGAGAGCCATAGTGTGCGGAGACCGGTGATGATGATGATGATGATG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTGCGGAGACCGGTGATGATGATGATGATGATG 180
Qy 181 GACGACCGGCTCTCTTCTTGTATCAACCGCTCAATAGCTGATGATGATGATGATGATG 240
Db 181 GACGACCGGCTCTCTTCTTGTATCAACCGCTCAATAGCTGATGATGATGATGATGATG 240
Qy 241 GCGAGACTGTAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Db 241 GCGAGACTGTAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Qy 301 GTGCTTCGAGTGCCTCCCGGAGAGTCTGTAGACCGTGCACATGAGCAATGCTTAAC 360
Db 301 GTGCTTCGAGTGCCTCCCGGAGAGTCTGTAGACCGTGCACATGAGCAATGCTTAAC 360
Qy 361 CTCAAAGAAAACCAAGGCGCGCCATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 CTCAAAGAAAACCAAGGCGCGCCATGATGATGATGATGATGATGATGATGATGATG 420
Qy 421 CGGCGCTTGGTGGAGAGGCTATGCGCTATGAGTGGGCAACAAGAAATCGGCTCT 480
Db 421 CGGCGCTTGGTGGAGAGGCTATGCGCTATGAGTGGGCAACAAGAAATCGGCTCT 480
Qy 481 CTGATGCGCGCTGTTCGCGCTGTCAAGCCAGGAGGCGCGCTTTTGTCAAGACCG 540
Db 481 CTGATGCGCGCTGTTCGCGCTGTCAAGCCAGGAGGCGCGCTTTTGTCAAGACCG 540
Qy 541 ACCTGTCCGGTGGCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
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Db 601 CGAGGCGGCTCTCTGCGAGCTGTCTGAGCTGTCACTCACTCACTCACTCACTCACT 660
Qy 661 TGGTATTGGGCGAAGTGGCGGGGCGAGAGTCTCTGATCACTTACTTCTCTGCGAGA 720
Db 661 TGGTATTGGGCGAAGTGGCGGGGCGAGAGTCTCTGATCACTTACTTCTCTGCGAGA 720
Qy 721 AAGTATCAATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 721 AAGTATCAATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 780

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Db	721	AAGTATCCATATATGCTGATGTCGAATTGGCGGGCTGCTGCAATTAGCGTTTGAATCCGGCTACTGCC	780
Qy	781	CATTGACCCACCAAGCGAAACATGCAATCGAGCGAGCAGCTACTCGGATGGAAGCCGGTTC	840
Db	781	CATTGACCCACCAAGCGAAACATGCAATCGAGCGAGCAGCTACTCGGATGGAAGCCGGTTC	840
Qy	841	TTGTGATCAGAGATGATGTGAGCAAGAGATCGAGGGGCTCGGCGCCAGGAGCTGTTGG	900
Db	841	TTGTGATCAGAGATGATGTGAGCAAGAGATCGAGGGGCTCGGCGCCAGGAGCTGTTGG	900
Qy	901	CCAGGCTCAGGCGCGCATGCGCGAGCGAGATCTCGTGTGACCCATGSCGATGCTT	960
Db	901	CCAGGCTCAGGCGCGCATGCGCGAGCGAGATCTCGTGTGACCCATGSCGATGCTT	960
Qy	961	GCTTCCCAATATATGATGTGAAATGAGCGGCTTTCTGATTCATGATGTGGCGGGC	1020
Db	961	GCTTCCCAATATATGATGTGAAATGAGCGGCTTTCTGATTCATGATGTGGCGGGC	1020
Qy	1021	TGGGTGTGCGGACCGCATATGAGACATAGCGTTGCTACCCGATATTTGTGAAGAGC	1080
Db	1021	TGGGTGTGCGGACCGCATATGAGACATAGCGTTGCTACCCGATATTTGTGAAGAGC	1080
Qy	1081	TTGGGAGGAAATGAGGCTGACCGCTTCCGCTTACGGATGCGCGGCTCCGATTCGC	1140
Db	1081	TTGGGAGGAAATGAGGCTGACCGCTTCCGCTTACGGATGCGCGGCTCCGATTCGC	1140
Qy	1141	AGCCGATGCTTCTATGCGCTTCTTGAAGATTTCTTGAATTTAAACAGCCACAGC	1200
Db	1141	AGCCGATGCTTCTATGCGCTTCTTGAAGATTTCTTGAATTTAAACAGCCACAGC	1200
Qy	1201	GTTTCCCTCTAGCGGAGATCAATTCGCGCCCTCCCTCCCGCCCGCCCTAGCTTACGCG	1260
Db	1201	GTTTCCCTCTAGCGGAGATCAATTCGCGCCCTCCCTCCCGCCCGCCCTAGCTTACGCG	1260
Qy	1261	CGAAGCCGCTTGGAATTAAGCGCGGCTGTGCTTGTATATGTTATTTCCACCATATTG	1320
Db	1261	CGAAGCCGCTTGGAATTAAGCGCGGCTGTGCTTGTATATGTTATTTCCACCATATTG	1320
Qy	1321	CGGTCTTTTGGCAATGTGTAGGGCCCGGAAACCTGCGCTGTCTCTTGAAGAGCATTTCT	1380
Db	1321	CGGTCTTTTGGCAATGTGTAGGGCCCGGAAACCTGCGCTGTCTCTTGAAGAGCATTTCT	1380
Qy	1381	AGGGGTCTTTCCTGCTGCGCAAAAGGAATGCAAGTCTGTGGAATGTGCGGAAGAGCA	1440
Db	1381	AGGGGTCTTTCCTGCTGCGCAAAAGGAATGCAAGTCTGTGGAATGTGCGGAAGAGCA	1440
Qy	1441	GTTCTCTGGAAGCTTCTTGAAGCAAAACAAGTCTGTAGCGACCTTTGACGACGCG	1500
Db	1441	GTTCTCTGGAAGCTTCTTGAAGCAAAACAAGTCTGTAGCGACCTTTGACGACGCG	1500
Qy	1501	AAACCCCGACGCTGAGGGAAGGTGCTGCGGCGCAAAAGCAGCTGTATGAATATACCT	1560
Db	1501	AAACCCCGACGCTGAGGGAAGGTGCTGCGGCGCAAAAGCAGCTGTATGAATATACCT	1560
Qy	1561	GCAAAAGCGCGCAACAACCCAGTGCACGTTGTGAGTTGATAGTTGTGGAAGAGTCAAA	1620
Db	1561	GCAAAAGCGCGCAACAACCCAGTGCACGTTGTGAGTTGATAGTTGTGGAAGAGTCAAA	1620
Qy	1621	TGGCTCTCTCCTCAAGGATTTCAACAAGGGGCTGAAGATGCGCCAGAAAGGTATCCCATTTGT	1680
Db	1621	TGGCTCTCTCCTCAAGGATTTCAACAAGGGGCTGAAGATGCGCCAGAAAGGTATCCCATTTGT	1680
Qy	1681	ATGGGATCTGATCTGGGGCTCTGCTGCAATGCTTTACATGTGTTTATGCGAGGTTAAAA	1740
Db	1681	ATGGGATCTGATCTGGGGCTCTGCTGCAATGCTTTACATGTGTTTATGCGAGGTTAAAA	1740
Qy	1741	AACGCTCTAGGCCCCCGCAACACAGGGGAGCTGTTTCTCTTGAAGAAACAGATATATCC	1800
Db	1741	AACGCTCTAGGCCCCCGCAACACAGGGGAGCTGTTTCTCTTGAAGAAACAGATATATCC	1800
Qy	1801	ATGCGGCTATTTAGGCGCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCT	1860
Db	1801	ATGCGGCTATTTAGGCGCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCATCT	1860
Qy	1861	AGCTCTACAGGCGCGGAGACAGGAGTGTGAGGGGAGTGTCAAGTGTGTCTCCACCGCA	1920
Db	1861	AGCTCTACAGGCGCGGAGACAGGAGTGTGAGGGGAGTGTCAAGTGTGTCTCCACCGCA	1920
Qy	1921	ACACATCTTTCTGAGCAGCTGCGCTCAATGAGCGTGTGTGACGTGTATCATGTGTGC	1980
Db	1921	ACACATCTTTCTGAGCAGCTGCGCTCAATGAGCGTGTGTGACGTGTGTATCATGTGTGC	1980
Qy	1981	GGCTCAAAAGACCTTGGCGCGCCAAAGGGCCCATACCCCAATGTATACCAATGTGAC	2040
Db	1981	GGCTCAAAAGACCTTGGCGCGCCAAAGGGCCCATACCCCAATGTATACCAATGTGAC	2040
Qy	2041	CAGGACCTGCTGCGCTGCAAGCGCGCCCGGGGGCGCTTCTTGAACACATGACCTGTC	2100
Db	2041	CAGGACCTGCTGCGCTGCAAGCGCGCCCGGGGGCGCTTCTTGAACACATGACCTGTC	2100
Qy	2101	GCGAGCTGGACCTTACTTGTGTACAGAGCATGCGATGTTCATTTCCGGTGCCTGGCGG	2160
Db	2101	GCGAGCTGGACCTTACTTGTGTACAGAGCATGCGATGTTCATTTCCGGTGCCTGGCGG	2160
Qy	2161	GCGCAGACAGGGGAGGAGCTACTCTCCCGCAGGCGCGCTCTCTATGGAAGGCTCTTGC	2220
Db	2161	GCGCAGACAGGGGAGGAGCTACTCTCCCGCAGGCGCGCTCTCTATGGAAGGCTCTTGC	2220
Qy	2221	GCGGCTCACTGTCTGTGCCCTCGAGGACAGCTGTGAGCACTTTCCGGGCTGCGTGTGC	2280
Db	2221	GCGGCTCACTGTCTGTGCCCTCGAGGACAGCTGTGAGCACTTTCCGGGCTGCGTGTGC	2280
Qy	2281	ACCCGAGGGGTTGCGAAGCGGTTGAGCTTTTACCCGCTGAGTGTATGGAACCATATG	2340
Db	2281	ACCCGAGGGGTTGCGAAGCGGTTGAGCTTTTACCCGCTGAGTGTATGGAACCATATG	2340
Qy	2341	CGGTCCCGGCTTACAGGACACACGCGCCCTCCGCGCGGACCGGAGCATTCGCAAGTG	2400
Db	2341	CGGTCCCGGCTTACAGGACACACGCGCCCTCCGCGCGGACCGGAGCATTCGCAAGTG	2400
Qy	2401	GCCCATCTACAGCGCCCTACTGTGAGGGCAAGAGCACTAAGTGTGCGGCTGCTATGCA	2460
Db	2401	GCCCATCTACAGCGCCCTACTGTGAGGGCAAGAGCACTAAGTGTGCGGCTGCTATGCA	2460
Qy	2461	GCCCAAGGATTAAGGTGTGTCTGTGAACCGGTGCGCGGACCCGATGAGTTGCGG	2520
Db	2461	GCCCAAGGATTAAGGTGTGTCTGTGAACCGGTGCGCGGACCCGATGAGTTGCGG	2520
Qy	2521	GCGTATATGTCTAAGGCACATGTATGCAACCTTAACATCAAGCCGGGTATGAGCACATC	2580
Db	2521	GCGTATATGTCTAAGGCACATGTATGCAACCTTAACATCAAGCCGGGTATGAGCACATC	2580
Qy	2581	ACCAGCGGTGCCCGCATCAGTACCCACATATGCAAGTCTTCTTCCGAGAGGTGTGC	2640
Db	2581	ACCAGCGGTGCCCGCATCAGTACCCACATATGCAAGTCTTCTTCCGAGAGGTGTGC	2640
Qy	2641		

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QY 2941 AAGCTGCGGCGCTGGAGTCAATGCTGAGCATATTACCGGGCGCTTATGATCCTGC 3000
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Db 2941 AAGCTGTCGGCCCTCGGAGTCAATGCTGAGCATATTACCGGGCGCTTATGATCCTGC 3000
QY 3001 ATACCACTAGCGGAGAGCTGATGTCGTAGCAAGGAGCGCTTATGAGCGGCTTTACC 3060
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Db 3001 ATACCACTAGCGGAGAGCTGATGTCGTAGCAAGGAGCGCTTATGAGCGGCTTTACC 3060
QY 3061 GGGCATTTGCACTGAGTCACTGAGTCAATGTCACACCGAGAGTGCAGCTTACG 3120
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Db 3061 GGGCATTTGCACTGAGTCACTGAGTCAATGTCACACCGAGAGTGCAGCTTACG 3120
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QY 3181 CAGCGGCGAGAGAGTGTAGAGGAGAGATGGGATTTACAGGTTTGTGACTCCAGAG 3240
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Db 3181 CAGCGGCGAGAGAGTGTAGAGGAGAGATGGGATTTACAGGTTTGTGACTCCAGAG 3240
QY 3241 GAAGGCGCCCTGGGCAATGTCGATTCCTCGGTTCTGTGCGAGTGTATGACGGGCTGT 3300
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Db 3241 GAAGGCGCCCTGGGCAATGTCGATTCCTCGGTTCTGTGCGAGTGTATGACGGGCTGT 3300
QY 3301 GCTTGTGACGAGCTCAGCGCCCGGAGAGACTCAGTTAGGTTGCGGGCTTACCTAAACAG 3360
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Db 3301 GCTTGTGACGAGCTCAGCGCCCGGAGAGACTCAGTTAGGTTGCGGGCTTACCTAAACAG 3360
QY 3361 CCAGGGTTGCCCGTCTGCCAGAGACCATCTGAGTTCTGGAGAGGCTCTTTACAGGCTCT 3420
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Db 3361 CCAGGGTTGCCCGTCTGCCAGAGACCATCTGAGTTCTGGAGAGGCTCTTTACAGGCTCT 3420
QY 3421 ACCGACATAGAGCGCCATTTCTGTGCTCCAGACTAAGAGAGAGAGAGACAACTCCCTAC 3480
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Db 3421 ACCGACATAGAGCGCCATTTCTGTGCTCCAGACTAAGAGAGAGAGAGACAACTCCCTAC 3480
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Db 3481 CTGGTAGCATACAGGCTAGCGGTGCGCCAGGCGCTCAGGCTCCATCCATGTTGGAG 3540
QY 3541 CAATGTGAGAGTGTCTCATACAGGCTAAGGCTAAGGCTGAGGGGCAAGCGCCCTGCG 3600
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QY 3721 GTCCTAGAGCTGCGCGCGCTATTGCTGACAAACAGAGCGAGCTGTGTCATTTGTGGCAG 3780
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Db 7921 TAGCTGTAAGGTCGGGAGCGGCTGACTGAGAGAGGCTGATAGAGGCTCTCTGAG 7980
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Db 7981 AGATCAAGT 7987
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RESULT 12

AAD25324 standard; cDNA; 7987 BP.

AAD25324;

12-MAR-2002 (first entry)

Hepatitis C virus (HCV) adaptive replicon VI cDNA mutant.

Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
 adaptive replicon VI; mutant; ss.

Hepatitis C virus.

OS Synthetic.

Location/Qualifiers

1801..7758

/product- "HCV adaptive replicon VI protein"

4642..5982

/product- "NS5A protein of HCV adaptive replicon VII"

FT

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FT /note= "CDS does not include both start and stop
FT codon"
FT /partial
FT replace (5336, G)
FT mutation
XX /tag- c
PN W0200189364-A2.
XX
XX 29-NOV-2001.
PD
XX
XX 23-MAY-2001: 2001MO-US16822.
PE
XX
XX 23-MAY-2000: 2000US-0576589.
PR
XX
XX (UNIW ) UNIV WASHINGTON.
PA
XX
XX Rice CM, Blight RJ;
PI
XX
XX WPI: 2002-066755/09.
DR
XX
XX P-FSDB: AAE15720, AAE15721.
DR
XX
XX Hepatitis C virus variants having greater transfection efficiency and
FT ability to survive subpassage; useful as a vaccine for immunizing
FT primate to the virus, comprise non-naturally occurring viral sequences
FT
PS Disclosure; Page 74-77; 174pp; English.
XX
XX The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop in vitro and in vivo assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets.
CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficiency replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays.
CC production of immunogenic HCV particles for vaccination, engineering of
CC attenuated or defective HCV derivatives as possible vaccine candidates, engineering of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) adaptive replicon VI cDNA mutant. This sequence
CC is generated by the mutation g to t at position 5336 of
CC HCVrepibaarman/Availi cDNA.
CC
XX
SO Sequence 7987 BP; 1646 A; 2368 C; 2243 G; 1730 T; 0 other;

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Query Match 99.7%; Score 7965.4; DB 24; Length 7987;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 7981; Conservative 0; Mismatches 6; Indels 2; Gaps 1.

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QY 1 GCCAGCCCCGATTTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60
    |||
Db 1 GCCAGCCCCGATTTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60
QY 61 TCTTACGCGAGAAAGCGCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCCCTCCAGGAC 120
    |||
Db 61 TCTTACGCGAGAAAGCGCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCCCTCCAGGAC 120

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QY 121 CCCCCCTCCGSGAGACCATAGTGTGCGAAACCGGTGTACACCGGAATTGCCAG 180
 Db 121 CCCCCCTCCGSGAGACCATAGTGTGCGAAACCGGTGTACACCGGAATTGCCAG 180
 QY 181 GACGACCGGGTCTCTTCTTGATCAACCCGCTCAATGCCGTGAGATTGGCGTCCGCC 240
 Db 181 GACGACCGGGTCTCTTCTTGATCAACCCGCTCAATGCCGTGAGATTGGCGTCCGCC 240
 QY 241 GCGAGACTGTAGCCGAGTAGTGTGGGTGCGGAAGGCGTTGTGTACTCCTGATAGG 300
 Db 241 GCGAGACTGTAGCCGAGTAGTGTGGGTGCGGAAGGCGTTGTGTACTCCTGATAGG 300
 QY 301 GTGCTTGCGAGTGTCCCGGAGAGTGTGAGACCGTGCACCATAGACAGCAATCTTAAC 360
 Db 301 GTGCTTGCGAGTGTCCCGGAGAGTGTGAGACCGTGCACCATAGACAGCAATCTTAAC 360
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 Db 361 CTCGAAGAAACCAAGGCGCGCATGATTGAACAAGATGGATTGGACACAGATTCTC 420
 QY 421 CCGCCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGACACAGCAATCGCTGCT 480
 Db 421 CCGCCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGACACAGCAATCGCTGCT 480
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 Db 481 CTGATGCGCCGCTTTCGCGCTGTAGCGCAGGGCGCCGCTTCTTTGTCAAGCG 540
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 Db 541 ACCGTGCGGTCCTCTGATGACTGACAGACAGGCGCGCTATCGTGGGTGCGCA 600
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 Db 601 CGACGCGCTTCTTCCGCTGTAGCGCAGGCTGTGCTACTGAACCGGGAAGGAGTGC 660
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 Db 661 TCGTATTGGGCAAGTGCAGGCGCAGATCTCTGTATCATCTACCTTGTCTGCGGAGA 720
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 Db 721 AAGTATCATCATGTGCTATGCAATGCGGCGGTGATACGCTTGAATCGGCTACCTGCC 780
 QY 781 CATTGACACCAAGCGGAACATGATGATGAGCAGACAGCAAGTGGATGAGAGCGGTC 840
 Db 781 CATTGACACCAAGCGGAACATGATGATGAGCAGACAGCAAGTGGATGAGAGCGGTC 840
 QY 841 TTGTGATAGAGATGATGTGAGCAAGATCATGAGGCGTCCGCGCAAGCTGTGCG 900
 Db 841 TTGTGATAGAGATGATGTGAGCAAGATCATGAGGCGTCCGCGCAAGCTGTGCG 900
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 Db 901 CCAGGCTCAAGGCGGATGCGCGAGCGGAGATCTGCTGCTGAGCCATGGCGATGCT 960
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 Db 1021 TGGGTGTGGGAGCGGCTATGAGACATAGCGTGGTACCCTGATATGCTGAAGAGC 1080
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 Db 1441 GTTTCCTCTGGAAGCTTCTTGAAGAACCAACGCTGTAGCGACCTTTGACGACGCG 1500
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 Db 1501 AACCCGCCACCTGGGAGAGTGTGCTGTGCGGCCCAAAAGCCAGCTATTAAGTACCT 1560
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 Db 1561 GCAAGGCGGCAACACCCAGTGCACGCTGTGAGTTGAGTGTGGAAGAGTCAAA 1620
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 Db 1621 TGGCTCTCCTCAAGGCTTTCAACAAGGCGCTGAAGATGCCCAAGAGTACCCATTGT 1680
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 Db 1861 AGCCTCAAGGCGGAGACAGAACCAAGTGAAGGAGAGTCCAGGTGTCTCCACCGCA 1920
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 Db 2161 GGCAGACAGAGGAGGAGCTACTCTGCTGCGGCGCGCTGCTTGAAGAGGCTCTTGC 2220
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 Db 2221 GGCAGCTCACTGCTCTGCTGCGGCGACGCTGTGAGGATCTTGTGAGGCTGCGCTGTC 2280
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Db 2821 GCTGTGTCCAGACTGAGAAATCCCTTTATGGAAGGACATCCCATCGAGACATC 2880
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Db 3001 ATACCACTAGCGAGAGAGTATTTGTGTAGCAAGGACGCTTAATGACGGCTTTTAC 3060
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Db 3061 GCGCATTTCCAGTCACTGATGATGACTGCAATGATGTGTACCCAGACAGTCACTTCA 3120
QY 3121 CTG6ACCCGACCTTACCATTTAGAGAGGACGCGTCCACAGAGCGGCTGTACGCTG 3180
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Db 3481 CTG6TACCATACAGGCTTACGAGTGTGCGCAGG6GCTCAGGCTCACTCCATCGTGGAC 3540
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Db 3721 GTCTTACAGCTGTGCGCGCTATGCTGTGACACAGGAGCGTGTGATTTGGGACAG 3780
QY 3781 ATCATCTTGTCCGGAAGGCGGCGCATCATCCGACAGG6AAGTCTTTACGG6GAGTTC 3840
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QY 4141 ACCCTCGTTTAACTCTG6G6GAGTGGTGGCGGCAACTTCTCTCCAGCGCT 4200
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QY	4501	GGTAAACAGCTGTCCCCACGCACTATGTGCTTGAGACGACGCTGCAGACGTGTCACT	4560
Db	4501	GGTAACACAGCTGTCCCCACGCACTATGTGCTTGAGACGACGCTGCAGACGTGTCACT	4560
QY	4561	CAGATCCTCTGTAGTGTATACCACTACACTACAGTGGCTGAAGAGAGCTTACACAGTGGATCAAC	4520
Db	4561	CAGATCCTCTGTAGTGTATACCACTACACTACAGTGGCTGAAGAGAGCTTACACAGTGGATCAAC	4520
QY	4621	GAGAGCTGTCCACGCGCACTGTCCCGGCTGTGGCTAAGAGATGTTTGGATTGGATATGC	4680
Db	4621	GAGAGCTGTCCACGCGCACTGTCCCGGCTGTGGCTAAGAGATGTTTGGATTGGATATGC	4680
QY	4741	GTCCCTCTTCTTCATGTAAACGTGGGTACAAGGGAGTCTGGCGGGGAGAGGCTATCG	4800
Db	4741	GTCCCTCTTCTTCATGTAAACGTGGGTACAAGGGAGTCTGGCGGGGAGAGGCTATCG	4800
QY	4801	CAAAACCACTGCCCATGTGGAGCACAGATCACCCGACATGTGMAAAAGTTCCATAGG	4860
Db	4801	CAAAACCACTGCCCATGTGGAGCACAGATCACCCGACATGTGMAAAAGTTCCATAGG	4860
QY	4861	ATCTGGGGGCTATGAGCACTGTAGTAAACAGTGGCATATTCATCCCATTAACGCGTAC	4920
Db	4861	ATCTGGGGGCTATGAGCACTGTAGTAAACAGTGGCATATTCATCCCATTAACGCGTAC	4920
QY	4921	ACCAAGGGCCCTGTGCACAGCCCTCCCGGCGCAAAATATCTAGGGCGCTGTGCGGGTG	4980
Db	4921	ACCAAGGGCCCTGTGCACAGCCCTCCCGGCGCAAAATATCTAGGGCGCTGTGCGGGTG	4980
QY	4981	GCTACTAGAGAGTACAGTGGAGGTTTACGCGGGTGGGGGATTTCCATAGTACGCGGATG	5040
Db	4981	GCTACTAGAGAGTACAGTGGAGGTTTACGCGGGTGGGGGATTTCCATAGTACGCGGATG	5040
QY	5041	ACCACTGACAACGTAAAGTCCCGTGTCAAGTTCGGGCCCCCGAAATTTCTTACAGAAATG	5100
Db	5041	ACCACTGACAACGTAAAGTCCCGTGTCAAGTTCGGGCCCCCGAAATTTCTTACAGAAATG	5100
QY	5101	GATGGGGTGGGTGGACAGAGTACGCTTCAGGCGTCAAAACCCCTCTACGGGAGAGATG	5160
Db	5101	GATGGGGTGGGTGGACAGAGTACGCTTCAGGCGTCAAAACCCCTCTACGGGAGAGATG	5160
QY	5161	ACATTTCTGTGGTGGGCTCAATCAATACCTGTGTGGGTCCAGCTCCATGCGAGCCGAA	5220
Db	5161	ACATTTCTGTGGTGGGCTCAATCAATACCTGTGTGGGTCCAGCTCCATGCGAGCCGAA	5220
QY	5221	CCGGAAGTACAGATGCTCACTTTCAGATGCTACCGAACCCTCCCAATTAAAGCGGAGACG	5280
Db	5221	CCGGAAGTACAGATGCTCACTTTCAGATGCTACCGAACCCTCCCAATTAAAGCGGAGACG	5280
QY	5281	GCTAAGGCTAGGCTGGGCGAGGGATCTCCCGCTCTTGGCAGGCTACATGCTAGCCAG	5340
Db	5281	GCTAAGGCTAGGCTGGGCGAGGGATCTCCCGCTCTTGGCAGGCTACATGCTAGCCAG	5340
QY	5341	CTGTCTGCGCCTTCTTGAAAGGCAAAATGACATACCCGCTCATGATCTCCCGGAGCGCTGAC	5400
Db	5341	CTGTCTGCGCCTTCTTGAAAGGCAAAATGACATACCCGCTCATGATCTCCCGGAGCGCTGAC	5400
QY	5401	CTCATCAGGCAACCTCTGTGGCGGACAGAAATGGGGGAAATATCACCCCGGTGGAG	5460
Db	5401	CTCATCAGGCAACCTCTGTGGCGGACAGAAATGGGGGAAATATCACCCCGGTGGAG	5460
QY	5461	TCAGAAATAAGTAGTAAATTTTGGACCTTTTGAGCGCGCTCCAAAGCGAGAGAGATGAG	5520
Db	5461	TCAGAAATAAGTAGTAAATTTTGGACCTTTTGAGCGCGCTCCAAAGCGAGAGAGATGAG	5520
QY	5521	AGGGAAGTATCCGTTCCGGGGAGATCTCGGAGAGTCCAGAAATTCCTCTGAGCATG	5580
Db	5521	AGGGAAGTATCCGTTCCGGGGAGATCTCGGAGAGTCCAGAAATTCCTCTGAGCATG	5580
QY	5581	CCCATATGTGGGACCCCGGATTTACAAACCTTCCACTTTTGAAGTCTCGAAGGACCCGGAC	5640

Db	5561	CCCAATATGGAGCACC	CCCGATTTCACAACCCCTCCACATGTTAGATCTCGTGAAGACC	CGGAC	5640
Qy	5641	TACATCCCTCCAGTGGATACACGGGTTCCATTGACCGCCCTGGCAAGGCCCTCCGATACCA			5700
Db	5641	TACATCCCTCCAGTGGATACACGGGTTCCATTGACCGCCCTGGCAAGGCCCTCCGATACCA			5700
Qy	5701	CCTCCACGAGGAAGAGGACGGTTGTCTCTGTGAGAAATCACTACCGTGTCTTCTGCTTGGC			5760
Db	5701	CCTCCACGAGGAAGAGGACGGTTGTCTCTGTGAGAAATCACTACCGTGTCTTCTGCTTGGC			5760
Qy	5761	GAGCTCCGACCAAAAGACCTTCGACACTCCGATCGTGGCCGTGGACAGCGGCACGCA			5820
Db	5761	GAGCTCCGACCAAAAGACCTTCGACACTCCGATCGTGGCCGTGGACAGCGGCACGCA			5820
Qy	5821	ACGACCTCTCTCTGACACGCCCCCTCCAGCAGAGGCGAGCGGGATCCGACGTTGAGTCGTAC			5880
Db	5821	ACGACCTCTCTCTGACACGCCCCCTCCAGCAGAGGCGAGCGGGATCCGACGTTGAGTCGTAC			5880
Qy	5881	TCCTCCATGCCCCCCCCCTTGAAGGGGAGACCGGGGAGATCCGATCTCAGCAGCGGCTTGG			5940
Db	5881	TCCTCCATGCCCCCCCCCTTGAAGGGGAGACCGGGGAGATCCGATCTCAGCAGCGGCTTGG			5940
Qy	5941	TCCTACCGTAAGCAGAGAGGCTAGTGAAGAGCTGTCTGTCTGATGTCTTCAACATAG			6000
Db	5941	TCCTACCGTAAGCAGAGAGGCTAGTGAAGAGCTGTCTGTCTGATGTCTTCAACATAG			6000
Qy	6001	ACAGGCGCCCGATCAGCGCATCGCTGGGAGAGAAACCACTGCCATCAATGCATG			6060
Db	6001	ACAGGCGCCCGATCAGCGCATCGCTGGGAGAGAAACCACTGCCATCAATGCATG			6060
Qy	6061	AGCAACTCTTTTGTCTCCCTCACAACAATTGTTATGTATGATCAACAATCTGCGACGCGCAAGC			6120
Db	6061	AGCAACTCTTTTGTCTCCCTCACAACAATTGTTATGTATGATCAACAATCTGCGACGCGCAAGC			6120
Qy	6121	CTGGCGCAGGAAGAGGTCACCTTTGACAGAGCTCCAGTCCCTGGAGACACACTACCGCGAC			6180
Db	6121	CTGGCGCAGGAAGAGGTCACCTTTGACAGAGCTCCAGTCCCTGGAGACACACTACCGCGAC			6180
Qy	6181	GTGCTCAAGGAGTGAAGGGGAGAGGGGTCACAGTTAAGGCTAAACTTCTATCCCTGGAG			6240
Db	6181	GTGCTCAAGGAGTGAAGGGGAGAGGGGTCACAGTTAAGGCTAAACTTCTATCCCTGGAG			6240
Qy	6241	GAAGCTCTTAAGCTGACGCCCCACATTTGGCCAGATCTAAATTTGGCTATGGGCGCAAG			6300
Db	6241	GAAGCTCTTAAGCTGACGCCCCACATTTGGCCAGATCTAAATTTGGCTATGGGCGCAAG			6300
Qy	6301	GACGTCGCGAACCCTATCCAGAAAGGCCGTTAACCAATCCGCTCCGCTGGAGAGACTTG			6360
Db	6301	GACGTCGCGAACCCTATCCAGAAAGGCCGTTAACCAATCCGCTCCGCTGGAGAGACTTG			6360
Qy	6361	CTGGAAGACACTGAGACACCAATTGACACCACCATCATGAGCAAAAATATAGSTTTTCTGC			6420
Db	6361	CTGGAAGACACTGAGACACCAATTGACACCACCATCATGAGCAAAAATATAGSTTTTCTGC			6420
Qy	6421	GTCCACACCAAGAAAGGGGGGCGGCAACCCAGCTCGGCTTATGTTATCCCAATTTGGG			6480
Db	6421	GTCCACACCAAGAAAGGGGGGCGGCAACCCAGCTCGGCTTATGTTATCCCAATTTGGG			6480
Qy	6481	GTTCTGTGTGCGAGAAAATGCCCCCTTACGATGTGTGTCTCCACCCTCCCTCAGGCCGTG			6540
Db	6481	GTTCTGTGTGCGAGAAAATGCCCCCTTACGATGTGTGTCTCCACCCTCCCTCAGGCCGTG			6540
Qy	6541	ATGGGCTCTTATATGGAATTCATATCTCTCTCTGACAGGGGTCGATCTCTGGTAT			6600
Db	6541	ATGGGCTCTTATATGGAATTCATATCTCTCTCTGACAGGGGTCGATCTCTGGTAT			6600
Qy	6601	GCTTGAAGAGGAAATGCCCCATGTGGCTTGCGATATGACACCCGCGTGTATGATCA			6660
Db	6601	GCTTGAAGAGGAAATGCCCCATGTGGCTTGCGATATGACACCCGCGTGTATGATCA			6660
Qy	6661	ACGGCTACTGAGATGACATCCGCTGTGGAGATCAATCTACCAATGTTGACTTGGCC			6720
Db	6661	ACGGCTACTGAGATGACATCCGCTGTGGAGATCAATCTACCAATGTTGACTTGGCC			6720

Dp	6661	ACGGTACTGAGATGACATCCGTTGTAGAGAGTCACTCCCAATGTTGTGACTTGATGGC	6720
Qy	6721	CCCGAAGCCAGACAGGCCCTAAAGTTCGCTCACAGAGCGGGCTTTACATCGGGGGCCCCCTG	6780
Dp	6722	CCCGAAGCCAGACAGGCCCTAAAGTTCGCTCACAGAGCGGGCTTTACATCGGGGGCCCCCTG	6780
Qy	6781	ACTAATTTAAAGGGGAGAACTGCGGCTATCGCCGGTCCCGGAGCGGGGTACTGACG	6840
Dp	6781	ACTAATTTAAAGGGGAGAACTGCGGCTATCGCCGGTCCCGGAGCGGGGTACTGACG	6840
Qy	6841	ACCAGCTCGCGTAATACCCCTCAATGTTACTTGAAGGCCCTGGGGCTGTGAGCTGCG	6900
Dp	6841	ACCAGCTCGCGTAATACCCCTCAATGTTACTTGAAGGCCCTGGGGCTGTGAGCTGCG	6900
Qy	6901	AACCTCCAGSAGCTGCGACGATGCTCGATGACGGAGACGACCTGTGTTATCTGGAAGC	6960
Dp	6901	AACCTCCAGSAGCTGCGACGATGCTCGATGACGGAGACGACCTGTGTTATCTGGAAGC	6960
Qy	6961	GCGGGGACCCAGAGAGCAGAGCGAGCCCTACGGGCCCTTCAGGAGGCTATGACTAGATAC	7020
Dp	6961	GCGGGGACCCAGAGAGCAGAGCGAGCCCTACGGGCCCTTCAGGAGGCTATGACTAGATAC	7020
Qy	7021	TCATGCCCCCTTGGGAGACCCGCCCAACACCAAGATACGATTTGGATTTGATTAACATCATGC	7080
Dp	7021	TCATGCCCCCTTGGGAGACCCGCCCAACACCAAGATACGATTTGGATTTGATTAACATCATGC	7080
Qy	7081	TCCCCCAATGTTCACATCGCGACGACGATGTCATGTGGCAAAAGGGTACTATCTCACCCGT	7140
Dp	7081	TCCCCCAATGTTCACATCGCGACGACGATGTCATGTGGCAAAAGGGTACTATCTCACCCGT	7140
Qy	7141	GACCCCAACACCCCTTGGCGGGGCTGCTGGTGGAGACACTAGACACATCTCCACTCAT	7200
Dp	7141	GACCCCAACACCCCTTGGCGGGGCTGCTGGTGGAGACACTAGACACATCTCCACTCAT	7200
Qy	7201	TCCGGCTAGGCAACATCATCATGATGTGGGCCACCTTGTGGCAAGATGATCTGTATG	7260
Dp	7201	TCCGGCTAGGCAACATCATCATGATGTGGGCCACCTTGTGGCAAGATGATCTGTATG	7260
Qy	7261	ACTCATTTCTTCTCCATCCTTTAGCTCAGGAACAATTGA AAAAGCCCTAGATTTGTACG	7320
Dp	7261	ACTCATTTCTTCTCCATCCTTTAGCTCAGGAACAATTGA AAAAGCCCTAGATTTGTACG	7320
Qy	7321	ATTCAGGGGGGCGCTGATCCATCATTTGAGCGCACTGAGCTACCTCCCATATTCATCAAGACTC	7380
Dp	7321	ATTCAGGGGGGCGCTGATCCATCATTTGAGCGCACTGAGCTACCTCCCATATTCATCAAGACTC	7380
Qy	7381	CATGGCCTTAGCGCATTTTCCACTCCATAGTTACTCTCCAGGTGAGATCATATAGGGTGGCT	7440
Dp	7381	CATGGCCTTAGCGCATTTTCCACTCCATAGTTACTCTCCAGGTGAGATCATATAGGGTGGCT	7440
Qy	7441	TCAATGCTCAGAGAACTTGGGGGTACCGCCCTTGCGAGTCTGGAGACATCGGGCCAGAACT	7500
Dp	7441	TCAATGCTCAGAGAACTTGGGGGTACCGCCCTTGCGAGTCTGGAGACATCGGGCCAGAACT	7500
Qy	7501	GTCGGCGCTAGGCTACTGTGCCAAGGGGGAGGGGCTGCACATTTGGCAAGTAACTCTTC	7560
Dp	7501	GTCGGCGCTAGGCTACTGTGCCAAGGGGGAGGGGCTGCACATTTGGCAAGTAACTCTTC	7560
Qy	7561	AACCTGCGAGTAAAGACCAAGCTCAAACTCACTCAATCCCGCTGCGCTCCACAGTTGGAT	7620
Dp	7561	AACCTGCGAGTAAAGACCAAGCTCAAACTCACTCAATCCCGCTGCGCTCCACAGTTGGAT	7620
Qy	7621	TTATCCAGCGGATCGTTGCTGTGGTTCAGAGGGGGAGACATATATACAGCCTGTCTGT	7680
Dp	7621	TTATCCAGCGGATCGTTGCTGTGGTTCAGAGGGGGAGACATATATACAGCCTGTCTGT	7680
Qy	7681	GCCGAGCCCGCTGTTCATGTGCTGCTACTCTACTTTCTGTAGGGTACGATCTAT	7740
Dp	7681	GCCGAGCCCGCTGTTCATGTGCTGCTACTCTACTTTCTGTAGGGTACGATCTAT	7740
Qy	7741	CTACTCCCAACCGATGAACGGGGAGCTAAACCTCCAGGCCAATATGGCATCTCGTTT	7800
Dp	7741	CTACTCCCAACCGATGAACGGGGAGCTAAACCTCCAGGCCAATATGGCATCTCGTTT	7800

[illegible]

QY 1 GCCAGCCCCGATTTGGGGGGGACACTCCACCATATGATCCTCCCTGTGAGAACTACTG 60
Db 1 GCCAGCCCCGATTTGGGGGGGACACTCCACCATATGATCCTCCCTGTGAGAACTACTG 60
QY 61 TCTTCAGAGAAAGCGTCTAGCCATGGGCTAGTATGATGATGCTGACGCTCCAGAC 120
Db 61 TCTTCAGAGAAAGCGTCTAGCCATGGGCTAGTATGATGATGCTGACGCTCCAGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACCGGAATTGGAC 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACCGGAATTGGAC 180
QY 181 GAGACCGGGTCTTCTTCTTGATCAACCCGCTCAATGCCGTGAGATTTGGGCGTGC 240
Db 181 GAGACCGGGTCTTCTTCTTGATCAACCCGCTCAATGCCGTGAGATTTGGGCGTGC 240
QY 241 GCGAGACTGCTAGCCAGTAGTGTGGGTGCGGAAGGCTTGTGTACTGCTGATAGG 300
Db 241 GCGAGACTGCTAGCCAGTAGTGTGGGTGCGGAAGGCTTGTGTACTGCTGATAGG 300
QY 301 GTGCTTGCAGATGCCCGGAGAGTCTGATAGCCGTGCACATGAGCAGATCCTAAG 360
Db 301 GTGCTTGCAGATGCCCGGAGAGTCTGATAGCCGTGCACATGAGCAGATCCTAAG 360
QY 361 CTCGAAGAAACCAAGAGGCGCGCATGATGAAACAGATGATGATGACGAGGTTCTC 420
Db 361 CTCGAAGAAACCAAGAGGCGCGCATGATGAAACAGATGATGATGACGAGGTTCTC 420
QY 421 CGGCGCTTGGGTGAGAGAGCTATTGCGCTATGACTGGGCAACAGACATCGCTACT 480
Db 421 CGGCGCTTGGGTGAGAGAGCTATTGCGCTATGACTGGGCAACAGACATCGCTACT 480
QY 481 CTGATCGCGCGTTCGCGCTGTGAGGCGAGGGCGCGGCTTCTTTGTCAGAACCG 540
Db 481 CTGATCGCGCGTTCGCGCTGTGAGGCGAGGGCGCGGCTTCTTTGTCAGAACCG 540
QY 541 ACCGTGCGGTCCTTGATGATGACGAGAGAGGAGCGCGCTATCGTGCTGGCCA 600
Db 541 ACCGTGCGGTCCTTGATGATGACGAGAGAGGAGCGCGCTATCGTGCTGGCCA 600
QY 601 CGACGGGCTTCTTCTGCGAGCTGTGTCAGACGTGTCTACGAGCGGAGAGGACTGCG 660
Db 601 CGACGGGCTTCTTCTGCGAGCTGTGTCAGACGTGTCTACGAGCGGAGAGGACTGCG 660
QY 661 TGCATTTGGGCGAAGTGCCTGGGGGAGATCTCTCTCATCTCACCTTGCTCTGCCAGA 720
Db 661 TGCATTTGGGCGAAGTGCCTGGGGGAGATCTCTCTCATCTCACCTTGCTCTGCCAGA 720
QY 721 AAGTATCCATGATGGCTGATGCAATGGCGGCGCTGACATACGCTTGATCCGCTACCTGCC 780
Db 721 AAGTATCCATGATGGCTGATGCAATGGCGGCGCTGACATACGCTTGATCCGCTACCTGCC 780
QY 781 CATTGCAACCAAGCGAAGCATGCGATGAGCGAGCAGTACTCGGATGGAAGCCGCTG 840
Db 781 CATTGCAACCAAGCGAAGCATGCGATGAGCGAGCAGTACTCGGATGGAAGCCGCTG 840
QY 841 TTGTGATGATGATGATGATGAGCAAGAGCATGAGGGCTGCGCCAGCCGAACTGTGG 900
Db 841 TTGTGATGATGATGATGATGAGCAAGAGCATGAGGGCTGCGCCAGCCGAACTGTGG 900
QY 901 CCAGGCTCAAGGCGGCGCATGCGCGAGCGAGATCTCGTGTGATGATGAGGATGCT 960
Db 901 CCAGGCTCAAGGCGGCGCATGCGCGAGCGAGATCTCGTGTGATGATGAGGATGCT 960
QY 961 GCTTGGCAATATCATGTGTGAAAAAGCGCTTTTGTGATTCATGACTGTGGCGGC 1020
Db 961 GCTTGGCAATATCATGTGTGAAAAAGCGCTTTTGTGATTCATGACTGTGGCGGC 1020
QY 1021 TGGGTGTGCGGAGCGCTATCAGGACATAGGCTTGGCTACCCGATGATTTGTGAGAGC 1080
Db 1021 TGGGTGTGCGGAGCGCTATCAGGACATAGGCTTGGCTACCCGATGATTTGTGAGAGC 1080
QY 1081 TTGGGGCGAATGGGCTGACCGGCTTCGTCGCTTTAGGATATGGCGCTCCGATTCG 1140
Db 1081 TTGGGGCGAATGGGCTGACCGGCTTCGTCGCTTTAGGATATGGCGCTCCGATTCG 1140
QY 1141 AGCGATGCGCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
Db 1141 AGCGATGCGCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTCCCTTACGGGATCAATTCGCGCCCTCTGCTCCCTCCCGCCCTAACGTTACTG 1260
Db 1201 GTTCCCTTACGGGATCAATTCGCGCCCTCTGCTCCCTCCCGCCCTAACGTTACTG 1260
QY 1261 CGAAGCGGCTTGAATTAAGCGGCTGTGCTGTTGCTATGATGATTTTCCACCAATG 1320
Db 1261 CGAAGCGGCTTGAATTAAGCGGCTGTGCTGTTGCTATGATGATTTTCCACCAATG 1320
QY 1321 CCGTCTTTGGCAATGTGAGGGCGCGGAACCTGGCCCTGCTCTTGACGAGATTCCT 1380
Db 1321 CCGTCTTTGGCAATGTGAGGGCGCGGAACCTGGCCCTGCTCTTGACGAGATTCCT 1380
QY 1381 AGGGTCTTTCCTCTCTGCGCAAGGAATGCAAGTCTGTGAATGTCTGTAAGAGCA 1440
Db 1381 AGGGTCTTTCCTCTCTGCGCAAGGAATGCAAGTCTGTGAATGTCTGTAAGAGCA 1440
QY 1441 GTTCCCTGGAAGCTTCTTGAAGACAAACAGTGTAGGACCTTTGACGACCGG 1500
Db 1441 GTTCCCTGGAAGCTTCTTGAAGACAAACAGTGTAGGACCTTTGACGACCGG 1500
QY 1501 AACCCCGCACCTGGGCGAAGGTGCTCTGCGGCCAAAAGCCAGCTGATAAGATACCT 1560
Db 1501 AACCCCGCACCTGGGCGAAGGTGCTCTGCGGCCAAAAGCCAGCTGATAAGATACCT 1560
QY 1561 GCAAGGGGCGCAACCCAGTGCACCTGTGATGATGATGATGATGATGATGATGATG 1620
Db 1561 GCAAGGGGCGCAACCCAGTGCACCTGTGATGATGATGATGATGATGATGATGATG 1620
QY 1621 TGGCTCTCCTCAAGCGTATTCAACAAGGGGTGAGAGTGGCCGAGAGTACCCATTGT 1680
Db 1621 TGGCTCTCCTCAAGCGTATTCAACAAGGGGTGAGAGTGGCCGAGAGTACCCATTGT 1680
QY 1681 ATGGGATCTGATCTGGGCTCTGGGCTGACATGCTTTACATGTGTTTGTGAGGTTAAA 1740
Db 1681 ATGGGATCTGATCTGGGCTCTGGGCTGACATGCTTTACATGTGTTTGTGAGGTTAAA 1740
QY 1741 AACGTCTAGGCCCCCGCAACAGGAGGAGCGGTTTTCCTTGAAGAAACAGATATAC 1800
Db 1741 AACGTCTAGGCCCCCGCAACAGGAGGAGCGGTTTTCCTTGAAGAAACAGATATAC 1800
QY 1801 ATGGGCTTATAGCGCTACTCTCCACAGACGCGAGGCTACTTGGCTGCATCATCT 1860
Db 1801 ATGGGCTTATAGCGCTACTCTCCACAGACGCGAGGCTACTTGGCTGCATCATCT 1860
QY 1861 ACCCTCACAGGCGGAGAGAACAGAGTGAAGGGAGGTCAGAGTGGCTCACCGCA 1920
Db 1861 ACCCTCACAGGCGGAGAGAACAGAGTGAAGGGAGGTCAGAGTGGCTCACCGCA 1920
QY 1921 ACACAATCTTTCTGGGACACTGCTGCTCAATGGCTGTGTTGAGCTGTCTATCATG 1980
Db 1921 ACACAATCTTTCTGGGACACTGCTGCTCAATGGCTGTGTTGAGCTGTCTATCATG 1980
QY 1981 GSGCTCAAGACCTTGGCGGCGCCAAAGGCGCCAAATTCACCAATGTACCAATGTG 2040
Db 1981 GSGCTCAAGACCTTGGCGGCGCCAAAGGCGCCAAATTCACCAATGTACCAATGTG 2040
QY 2041 CAGGACTCTGCTGAGCAAGCGCCCGGCGGCTTCTTGAACCATGACCTG 2100
Db 2041 CAGGACTCTGCTGAGCAAGCGCCCGGCGGCTTCTTGAACCATGACCTG 2100
QY 2101 GGCAGCTGGAACCTTTACTTGTGTACAGAGCATGCGCATGTCTTCGCGGCGCG 2160
Db 2101 GGCAGCTGGAACCTTTACTTGTGTACAGAGCATGCGCATGTCTTCGCGGCGCG 2160
QY 2161 GCGCAGCAGAGGGGAGCTACTCTCCAGGCGCTCTCTACTTGAAGGCGCTCTG 2220

Db 2161 GGGAGAGCAGGGGGAGCCCTACTCTCCCCAGGCCGCTCTCTACTGTGAAGGGCTCTTCG 2220
QY 2221 GGGGGTCCACTGCTCTGCCCTTCGGGGACGCTGTGGGATCTTTCCGGGCTTCCGCTGTC 2280
Db 2221 GGGGGTCCACTGCTCTGCCCTTCGGGGACGCTGTGGGATCTTTCCGGGCTTCCGCTGTC 2280
QY 2281 ACCCGAGGGGTGCGAAGGGGGTGGAGCTTGTACCCGTGAGTCTATGGAACCACTATG 2340
Db 2281 ACCCGAGGGGTGCGAAGGGGGTGGAGCTTGTACCCGTGAGTCTATGGAACCACTATG 2340
QY 2341 CGGTCCCGGCTTTCACGGACAACTCGTCCCTCCGGCGCTACCGAGCAATTCAGGGTG 2400
Db 2341 CGGTCCCGGCTTTCACGGACAACTCGTCCCTCCGGCGCTACCGAGCAATTCAGGGTG 2400
QY 2401 GCCCATCTACAGCCCCCTACTGCTAGGGGAGAGCACTAAGGTGGCGGCTCGTATGCA 2460
Db 2401 GCCCATCTACAGCCCCCTACTGCTAGGGGAGAGCACTAAGGTGGCGGCTCGTATGCA 2460
QY 2461 GCCCAAGGGTATAAGGTGCTTGTCTGMAACCGTCCGTGCGGCCACCTAGGTTTCGGG 2520
Db 2461 GCCCAAGGGTATAAGGTGCTTGTCTGMAACCGTCCGTGCGGCCACCTAGGTTTCGGG 2520
QY 2521 GCGTATATGTCTAAGGACATGATGACCTACCATGAGTTCCTTCCGACGAGTTCG 2580
Db 2521 GCGTATATGTCTAAGGACATGATGACCTACCATGAGTTCCTTCCGACGAGTTCG 2580
QY 2581 ACCAGGGGTGCCCCCATACGCTACTCCACCTATGGCAAGTTCCTTCCGACGAGTTCG 2640
Db 2581 ACCAGGGGTGCCCCCATACGCTACTCCACCTATGGCAAGTTCCTTCCGACGAGTTCG 2640
QY 2641 TCTGGGGGGCGCTTGCATCATATATGTGATGAGTGGCCACTCAGCACTGACCTGACCACT 2700
Db 2641 TCTGGGGGGCGCTTGCATCATATATGTGATGAGTGGCCACTCAGCACTGACCTGACCACT 2700
QY 2701 ATCTGGGACATCGGCACAGTCTCTGAGACAGCGAGAGCGGCTGGAGCGGACTCGTCTG 2760
Db 2701 ATCTGGGACATCGGCACAGTCTCTGAGACAGCGAGAGCGGCTGGAGCGGACTCGTCTG 2760
QY 2761 CTGCGCACCGCTACGCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGGGAGTG 2820
Db 2761 CTGCGCACCGCTACGCTCCGGGATCGGTACCGTGCACATCCAAACATCGAGGGAGTG 2820
QY 2821 GCTGTGTCCAGCACTGGAGAAATCCCTTTATGGCAAGCACTCCCATCGAGACATC 2880
Db 2821 GCTGTGTCCAGCACTGGAGAAATCCCTTTATGGCAAGCACTCCCATCGAGACATC 2880
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Db 2881 AAGGGGGGAGGACACTTCATTTTCTGCCATTCAGAGAAATGTGATGAGTTCGCGCGG 2940
QY 2941 AAGGTGTCCGGCTCGGACATGATGCTGTAGCATATTAACGGGGGCTTGAATGATCCGTC 3000
Db 2941 AAGGTGTCCGGCTCGGACATGATGCTGTAGCATATTAACGGGGGCTTGAATGATCCGTC 3000
QY 3001 ATACCACTAGCGGAGAGCTATGTGTAGCAACGAGACCTCTAATGAGGGGCTTTAC 3060
Db 3001 ATACCACTAGCGGAGAGCTATGTGTAGCAACGAGACCTCTAATGAGGGGCTTTAC 3060
QY 3061 GGGGATTCGACTCGTATGACTGCAATGATGTGTCCAGGAGTTCGACTTCAGC 3120
Db 3061 GGGGATTCGACTCGTATGACTGCAATGATGTGTCCAGGAGTTCGACTTCAGC 3120
QY 3121 CTGAGCCGACCTTCACCAATTGAGACGACGCTGCCACAAGACGGGTGTACGCTG 3180
Db 3121 CTGAGCCGACCTTCACCAATTGAGACGACGCTGCCACAAGACGGGTGTACGCTG 3180
QY 3181 CAGCGGCGAGAGACACTGTGTAGGGGAGATGGGCAATTAACAGGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGCGAGAGACACTGTGTAGGGGAGATGGGCAATTAACAGGTTTGTGACTCCAGGA 3240
QY 3241 GAACGGCCCTCGGCACTTTCGATTCCTCGGTTCTGTGCGATGCTATGACGGCGGCTGT 3300
Db 3241 GAACGGCCCTCGGCACTTTCGATTCCTCGGTTCTGTGCGATGCTATGACGGCGGCTGT 3300

Db 3241 GAACGGCCCTCGGCACTTTCGATTCCTCGGTTCTGTGCGATGCTATGACGGCGGCTGT 3300
QY 3301 GCTTGTAGAGCTCACAGCCCGCCAGAGCTCAGTTAGTTGCGGGCTTACTTAACACACA 3360
Db 3301 GCTTGTAGAGCTCACAGCCCGCCAGAGCTCAGTTAGTTGCGGGCTTACTTAACACACA 3360
QY 3361 CAGGGGTGCGGCTTCGACAGACCATCTGAGATCTGTGGGAAGGGCTCTTTACAGGCTC 3420
Db 3361 CAGGGGTGCGGCTTCGACAGACCATCTGAGATCTGTGGGAAGGGCTCTTTACAGGCTC 3420
QY 3421 ACCCATATAGCCCATTTCTTCCAGACTACAGGACGAGAGCACTTCCCTTAC 3480
Db 3421 ACCCATATAGCCCATTTCTTCCAGACTACAGGACGAGAGCACTTCCCTTAC 3480
QY 3481 CTGCTAGCATACAGGCTACGGTGTGCGGAGGCTCAGGCTTCACCTCCATCTGGGAC 3540
Db 3481 CTGCTAGCATACAGGCTACGGTGTGCGGAGGCTCAGGCTTCACCTCCATCTGGGAC 3540
QY 3541 CAATGTGSAAGTGTCTCATAGGGCTAAAGCCCTACGCTCAGGGCCAGGCCCTGTG 3600
Db 3541 CAATGTGSAAGTGTCTCATAGGGCTAAAGCCCTACGCTCAGGGCCAGGCCCTGTG 3600
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Db 3601 TATAGGCTGGAGCCGTTTCAAAACAGGTTTACTACACACACCCCATACCAATATACATC 3660
QY 3661 ATGCGATGCACTGTGGCTGACCTGAGAGTGTCTACAGACACCTGGGTGGAGGCGGA 3720
Db 3661 ATGCGATGCACTGTGGCTGACCTGAGAGTGTCTACAGACACCTGGGTGGAGGCGGA 3720
QY 3721 GTCTAGCAGCTCTGCGCGGCTATTGCTGTACACAGGACGCTGTGCTATGCTGGGACG 3780
Db 3721 GTCTAGCAGCTCTGCGCGGCTATTGCTGTACACAGGACGCTGTGCTATGCTGGGACG 3780
QY 3781 ATCATCTTGTCCGGAAGCCGGCCATCATCTCCGACAGAGGAATCCCTTTACCGGGAGTTC 3840
Db 3781 ATCATCTTGTCCGGAAGCCGGCCATCATCTCCGACAGGGAATCCCTTTACCGGGAGTTC 3840
QY 3841 GATGAGATGAGAGATGCGGCTCACACCTCCTTTACATCGAAGGGAATGCACTGCGC 3900
Db 3841 GATGAGATGAGAGATGCGGCTCACACCTCCTTTACATCGAAGGGAATGCACTGCGC 3900
QY 3901 GAACATTTCAACGAGAGGCAATGGGTGCTGCAAAACACCCCAAGCAAGCGGAGGCT 3960
Db 3901 GAACATTTCAACGAGAGGCAATGGGTGCTGCAAAACACCCCAAGCAAGCGGAGGCT 3960
QY 3961 GCTGTCCCGTGTGGAATCAAGTGGGAGACCTCGAAGCCTTCTGGGGGAAGCATATG 4020
Db 3961 GCTGTCCCGTGTGGAATCAAGTGGGAGACCTCGAAGCCTTCTGGGGGAAGCATATG 4020
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Db 4021 TGAATTTCAACGCGGATTCATATTTAGCAGGCTTGTCCACTGCTGCTGCAACCC 4080
QY 4081 GCGATGACACTAGTATGAGCACTTACAGCCTCTATCACAGCCCTATCACAGCCGCTCACACCAACAT 4140
Db 4081 GCGATGACACTAGTATGAGCACTTACAGCCTCTATCACAGCCCTATCACAGCCGCTCACACCAACAT 4140
QY 4141 ACCCTCTGTTTAACTCTCGGGGAGATGGGTGCGGCCCACTGTGCTCTCCAGCGCT 4200
Db 4141 ACCCTCTGTTTAACTCTCGGGGAGATGGGTGCGGCCCACTGTGCTCTCCAGCGCT 4200
QY 4201 GCTTGTGCTTGTGAGGCGCGGATGCGCTGGAGCGGCTGTGGACATAGGCTTGGG 4260
Db 4201 GCTTGTGCTTGTGAGGCGCGGATGCGCTGGAGCGGCTGTGGACATAGGCTTGGG 4260
QY 4261 AAGGTGCTTGTGATATTTTGGCAGGTTATGAGCAGAGGGGTGAGCGGCTGTGGCC 4320
Db 4261 AAGGTGCTTGTGATATTTTGGCAGGTTATGAGCAGAGGGGTGAGCGGCTGTGGCC 4320
QY 4321 TTTAAGGTCATGAGGCGGAGATGCCCTCCACGAGGACCTGGTTAACTACTTCCCTGCT 4380
Db 4321 TTTAAGGTCATGAGGCGGAGATGCCCTCCACGAGGACCTGGTTAACTACTTCCCTGCT 4380

QY	4381	ATCTCTCCCTTGAGCCCTTAGTGTGTGGGGTGTGTGTGCGACAGCATACTGCTGTGGCAC	4440
Db	4381	ATCTCTCCCTTGAGCCCTTAGTGTGTGGGGTGTGTGTGCGACAGCATACTGCTGTGGCAC	4440
QY	4441	GTGGGCCAGAGGGAGGGGCGCTGTGCAGTGGATGAACCGGCTATAGCTTGCTGTGGG	4500
Db	4441	GTGGGCCAGAGGGAGGGGCGCTGTGCAGTGGATGAACCGGCTATAGCTTGCTGTGGG	4500
QY	4501	GGTAAACAGCTCTCCCCACAGCACTATGTGCTGAGAGCGAGCGCTGACACGTGTCACT	4560
Db	4501	GGTAAACAGCTCTCCCCACAGCACTATGTGCTGAGAGCGAGCGCTGACACGTGTCACT	4560
QY	4561	CAGATCTCTCTAGTCTTAAACATCACTACGTGCTGTAAGAGGCTTCACACAGTGAAC	4620
Db	4561	CAGATCTCTCTAGTCTTAAACATCACTACGTGCTGTAAGAGGCTTCACACAGTGAAC	4620
QY	4621	GAGAGCTGTCCACAGCGCATGCTCCGGCTGTGGGCTAAAGAGATTTGGGATTTGATATGC	4680
Db	4621	GAGAGCTGTCCACAGCGCATGCTCCGGCTGTGGGCTAAAGAGATTTGGGATTTGATATGC	4680
QY	4681	ACGGTGTGACTGATTTCAAGAGCTGGCTCCAGTCCAAAGTCTCTCCCGATTTGGCGGGA	4740
Db	4681	ACGGTGTGACTGATTTCAAGAGCTGGCTCCAGTCCAAAGTCTCTCCCGATTTGGCGGGA	4740
QY	4741	GTCCCTCTTCTTCATAGTCAACGTGGGTACAGAGAGTGTGGCGGGGCGAGGCACTATG	4800
Db	4741	GTCCCTCTTCTTCATAGTCAACGTGGGTACAGAGAGTGTGGCGGGGCGAGGCACTATG	4800
QY	4801	CAAAACCACTGCCATGTGAGACAGATCCACCGGACATGTAAAAAAA---GGTTCATG	4857
Db	4801	CAAAACCACTGCCATGTGAGACAGATCCACCGGACATGTAAAAAAA---GGTTCATG	4857
QY	4858	AGGATGCTGGGGGCTAGAGCTCTACTATACAGTGGCATGGAACATTTCCCATTAAGCG	4917
Db	4861	AGGATGCTGGGGGCTAGAGCTCTACTATACAGTGGCATGGAACATTTCCCATTAAGCG	4920
QY	4918	TACACACAGGGGCCCTTGACAGCCCTCCCGGCGCCAAATTAATTCAGAGGCGCTGTGGCG	4977
Db	4921	TACACACAGGGGCCCTTGACAGCCCTCCCGGCGCCAAATTAATTCAGAGGCGCTGTGGCG	4980
QY	4978	GTGCTCTCTAGAGATACAGTGAAGGTTAGCGGGGTGGGGAATTTCCACTAGCTAACGGCG	5037
Db	4981	GTGCTCTCTAGAGATACAGTGAAGGTTAGCGGGGTGGGGAATTTCCACTAGCTAACGGCG	5040
QY	5038	ATGACCACTGACAAAGTCCCGCTGTCAAGTTCGCGGCCCGGAATTTCTTACAGAA	5097
Db	5041	ATGACCACTGACAAAGTCCCGCTGTCAAGTTCGCGGCCCGGAATTTCTTACAGAA	5100
QY	5098	GTGATGGGGGTGGGTTGSCAGAGTACGGTCCAGCGTGAACCCCTCTACGGGAGAG	5157
Db	5101	GTGATGGGGGTGGGTTGSCAGAGTACGGTCCAGCGTGAACCCCTCTACGGGAGAG	5160
QY	5158	GTACATTTCTGTGGGCTCAATCAATACCTGTGTGGGTACAGCTCCATGTGACGCC	5217
Db	5161	GTACATTTCTGTGGGCTCAATCAATACCTGTGTGGGTACAGCTCCATGTGACGCC	5220
QY	5218	GAAACGAGAGTGAAGTGTCACTTCCATGTCACGAGCCCTCCCATTAAGCGGAG	5277
Db	5221	GAAACGAGAGTGAAGTGTCACTTCCATGTCACGAGCCCTCCCATTAAGCGGAG	5280
QY	5278	ACGGCTAAGGCTAGGCTGTGGCAGGGAGTCTCCCCCTCTTGTGGCAGCTCAATGCACTAGC	5337
Db	5281	ACGGCTAAGGCTAGGCTGTGGCAGGGAGTCTCCCCCTCTTGTGGCAGCTCAATGCACTAGC	5340
QY	5338	CAGTGTCTGGGCTTCTCTTGAAGGGAACATGACATACCGGTCAATGATCCCGGAGCT	5397
Db	5341	CAGTGTCTGGGCTTCTCTTGAAGGGAATATGACATACCGGTCAATGATCCCGGAGCT	5400
QY	5398	GACCTCATCGAGGCCAACTCTGTGTGGGCGCAGAGATGGCGGGAGATCAACCCGCGTG	5457
Db	5401	GACCTCATCGAGGCCAACTCTGTGTGGGCGCAGAGATGGCGGGAGATCAACCCGCGTG	5460

QY	5458	GAGTCGAAAAATAAGTAGTAAATTGTTGGACTCTTTGAGCCGCTCCACGCGAGAGAGAT	5517
Db	5461	GAGTCGAAAAATAAGTAGTAAATTGTTGGACTCTTTGAGCCGCTCCACGCGAGAGAGAT	5520
QY	5518	GAGAGGGAAGATACCGTTCCGCGGAGATCCTGCGAGGCTCCAGAAATTCCTCGAGCG	5577
Db	5521	GAGAGGGAAGATACCGTTCCGCGGAGATCCTGCGAGGCTCCAGAAATTCCTCGAGCG	5580
QY	5578	ATGCCCATATGGGCGAGCGCCGGATTTACAACTCCACTGTTAGAGTCTTGGAAAGACCGG	5633
Db	5581	ATGCCCATATGGGCGAGCGCCGGATTTACAACTCCACTGTTAGAGTCTTGGAAAGACCGG	5644
QY	5638	GACTACCTCCCTCCAGTGTATACAGGGGTGTCCATTCCGCCCTCCCAAGGCCCTCCGATA	5697
Db	5641	GACTACCTCCCTCCAGTGTATACAGGGGTGTCCATTCCGCCCTCCCAAGGCCCTCCGATA	5700
QY	5698	CCACTCTCCAGGAGGAGAGAGAGGTTGTCCTCTCAGATATCAAGTGTCTTCGCTTG	5755
Db	5701	CCACTCTCCAGGAGGAGAGAGGTTGTCCTCTCAGATATCAAGTGTCTTCGCTTG	5766
QY	5758	GCGAGAGCTCCACAAAGACCTTCGCGAGCTCGAATCGTCGCGCCGTCCAGACGCGCAGC	5817
Db	5761	GCGAGAGCTCCACAAAGACCTTCGCGAGCTCGAATCGTCGCGCCGTCCAGACGCGCAGC	5820
QY	5818	GCAACGGCTCTCTCTGTGACAGCCCTCCGAGAGGGGAGAGGCGAGATCCGAGCTTAGTGC	5877
Db	5821	GCAACGGCTCTCTCTGTGACAGCCCTCCGAGAGGGGAGAGGCGAGATCCGAGCTTAGTGC	5880
QY	5878	TACTCTCCATGCCCCCTTTGAGGGGGAGCCGGGGGATCCGATTCAGCGACGGGTCT	5937
Db	5881	TACTCTCCATGCCCCCTTTGAGGGGGAGCCGGGGGATCCGATTCAGCGACGGGTCT	5944
QY	5938	TGTGCTACCCGAAGCGAGGAGGTAGTGAAGAGCTGCTGTGCGTCCGATGTCTACACA	5997
Db	5941	TGTGCTACCCGAAGCGAGGAGGTAGTGAAGAGCTGCTGTGCGTCCGATGTCTACACA	6000
QY	5998	TGGACAGGCGCCCTGATCACGCCATGGCGTGGGAGGAAACCAAGCTGCCATCAATGCA	6055
Db	6001	TGGACAGGCGCCCTGATCACGCCATGGCGTGGGAGGAAACCAAGCTGCCATCAATGCA	6066
QY	6058	CTGAGCACTCTTTGGCTCCGCTCACACAAATTTGCTATAGCTACACATCTCGACGCGA	6111
Db	6061	CTGAGCACTCTTTGGCTCCGCTCACACAAATTTGCTATAGCTACACATCTCGACGCGA	6122
QY	6118	AGCTCGCGCAGAAGANGTACCTTTGACAGACTCCAGTCTGAGACACACTACCGG	6177
Db	6121	AGCTCGCGCAGAAGANGTACCTTTGACAGACTCCAGTCTGAGACACACTACCGG	6180
QY	6178	GACCTGCTCAAGGATGAGAGGGAAGGCGTCACAGTTAAGGCTAACTTCTATCCGCG	6233
Db	6181	GACCTGCTCAAGGATGAGAGGGAAGGCGTCACAGTTAAGGCTAACTTCTATCCGCG	6244
QY	6238	GAGGAAAGCTGTAAAGTACTGACGCCCCACATTTGGCCAGATCTAAATTGGCTATGGGCA	6297
Db	6241	GAGGAAAGCTGTAAAGTACTGACGCCCCACATTTGGCCAGATCTAAATTGGCTATGGGCA	6300
QY	6298	AAGAGCTCCGGAACCTATCCAGCAAGGCGTTAACACATCCGCTCCGCTGGTGGAGAC	6355
Db	6301	AAGAGCTCCGGAACCTATCCAGCAAGGCGTTAACACATCCGCTCCGCTGGTGGAGAC	6366
QY	6358	TTGCTGGAAGACTGTGACACCAATTGACACCAATCATGGCAAAAAATGAGGTTTC	6411
Db	6361	TTGCTGGAAGACTGTGACACCAATTTGACACCAATCATGGCAAAAAATGAGGTTTC	6420
QY	6418	TGCCTCAACACAGAGAGGGGGCGCAACCAACAGCTGCTTTACTATTCAGATTGG	6477
Db	6421	TGCCTCAACACAGAGAGGGGGCGCAACCAACAGCTGCTTTACTATTCAGATTGG	6480
QY	6478	GGGCTGTGTGTCTCGAGAAATAGGCCCTTTACGATGTGTCTCACCTCCCTCAGGCG	6533
Db	6481	GGGCTGTGTGTCTCGAGAAATAGGCCCTTTACGATGTGTCTCACCTCCCTCAGGCG	6544
QY	6538	GTAATGGGCTCTTCATACGGAATTCATAATCTCTCGAGAGGAGGAGTCCAGTTCCTGAG	6597

Db 5541 GTATGATGGGCTTCATACAGGATTCACATCTCTCCTGGACACAGGGGTGAGAGTTCCTGGTG 6600
QY 6598 AATGCTGGAAAGCGAAGAAATGCGCTATGGCTTCGCATATGACACCCGCTGTTTAC 6657
Db 6601 AATGCTGGAAAGCGAAGAAATGCGCTATGGCTTCGCATATGACACCCGCTGTTTAC 6660
QY 6658 TCACGCTACTAGAAATGACATCCGTTGTGAGAGTCAATCTACCAATGTTGTACTG 6717
Db 6661 TCACGCTACTAGAAATGACATCCGTTGTGAGAGTCAATCTACCAATGTTGTACTG 6720
QY 6718 GCGCCCGAAGCCAGACAGGCGCATAGGTGCTCAGACAGCGGCTTTACATGGGGGCC 6777
Db 6721 GCGCCCGAAGCCAGACAGGCGCATAGGTGCTCAGACAGCGGCTTTACATGGGGGCC 6780
QY 6778 CTGACTAATCTAAAGGGAGAACTGGGCTATCGCGGTGCGCGGAGGGGTACTG 6837
Db 6781 CTGACTAATCTAAAGGGAGAACTGGGCTATCGCGGTGCGCGGAGGGGTACTG 6840
QY 6838 ACACACAGCTGGCGTAAATACCTCACAATGTTAAAGCGCGCTGGCGCTGTGAGCT 6897
Db 6841 ACACACAGCTGGCGTAAATACCTCACAATGTTAAAGCGCGCTGGCGCTGTGAGCT 6900
QY 6898 GCGAGCTCAGAGCTGCAGATGCTCGTATGCGGAGAGAGCTGTGTTATCTGTGA 6957
Db 6901 GCGAGCTCAGAGCTGCAGATGCTCGTATGCGGAGAGAGCTGTGTTATCTGTGA 6960
QY 6958 AGCGCGGGAGCCACAGAGAGAGAGAGCGAGCTACGCGGCTTCACGAGAGCTATGACTGA 7017
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QY 7018 TACTGTGCGCGCGCGGGAGCCCGCCCAACAGAAATAGAGTTGAGATGATTAACATCA 7077
Db 7021 TACTGTGCGCGCGCGGGAGCCCGCCCAACAGAAATAGAGTTGAGATGATTAACATCA 7080
QY 7078 TGCTCTCCATGTGTCACTGCGGCGAGATGATCTGCGAAAGGGTGTACTATCTCAC 7137
Db 7081 TGCTCTCCATGTGTCACTGCGGCGAGATGATCTGCGAAAGGGTGTACTATCTCAC 7140
QY 7138 CGTGACCCACACACCCCTTGCGGGGCTGGTGAGAGAGCTAGACACTCTCACTC 7197
Db 7141 CGTGACCCACACACCCCTTGCGGGGCTGGTGAGAGAGCTAGACACTCTCACTC 7200
QY 7198 AATTCTGCTAGGACAATCATCATGATGATGCGCCACCTTGCGGCAAGATGATCTG 7257
Db 7201 AATTCTGCTAGGACAATCATCATGATGATGCGCCACCTTGCGGCAAGATGATCTG 7260
QY 7258 ATGACATCTTCTTCTCCATCTCTTACGCTCAGAGAACACTTGAAAAAGCCCTAGATTGT 7317
Db 7261 ATGACATCTTCTTCTCCATCTCTTACGCTCAGAGAACACTTGAAAAAGCCCTAGATTGT 7320
QY 7318 CAGATCTAGCGGCGCTGTATCTACCTATGAGCACTGACCTACCTCAGATCTTCAAGCA 7377
Db 7321 CAGATCTAGCGGCGCTGTATCTACCTATGAGCACTGACCTACCTCAGATCTTCAAGCA 7380
QY 7378 CTCATGCGCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTG 7437
Db 7381 CTCATGCGCTTAGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTG 7440
QY 7438 GCTTCATGCTCAGAAACTTGGGTAACCGCCCTTGCGAGTGTGAGACATGCGGCCAGA 7497
Db 7441 GCTTCATGCTCAGAAACTTGGGTAACCGCCCTTGCGAGTGTGAGACATGCGGCCAGA 7500
QY 7498 AGTGTCCGCGCTAGGCTACTGTCCAGGGGGAGGGGCGCTCCACTGTGTGCAAGTACCTC 7557
Db 7501 AGTGTCCGCGCTAGGCTACTGTCCAGGGGGAGGGGCGCTGTGCAAACTGTGTGCAAGTACCTC 7560
QY 7558 TTCACTAGGCGAGTAAGAGACGTCAAACATCACTCCAGCTCCGCGCTCCAGCTG 7617
Db 7561 TTCACTAGGCGAGTAAGAGACGTCAAACATCACTCCAGCTCCGCGCTCCAGCTG 7620
QY 7618 GATTATCCAGCTGTGCTGTGCTGTACAGCGGGGGAGACATATATCCAGCCTGTCT 7677

Db 7621 GATTATCCAGCTGTGCTGTGCTGTACAGCGGGGAGACATATATCCAGCCTGTCT 7680
QY 7678 CGTGCCGAGCCCGCTGTGCTATGAGTCCACTCCACTTCTGTAGGGGTAGGCATC 7737
Db 7681 CGTGCCGAGCCCGCTGTGCTATGAGTCCACTCCACTTCTGTAGGGGTAGGCATC 7740
QY 7738 TATCTACTCCCAACCCAGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGT 7797
Db 7741 TATCTACTCCCAACCCAGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGT 7800
QY 7798 TTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTT 7857
Db 7801 TTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTT 7860
QY 7858 TTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTT 7917
Db 7861 TTTTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTT 7920
QY 7918 GCGTACGTGGAAGGTCCGTAGCCCTTGACTGCAAGAGTCTGATGAGCTCTC 7977
Db 7921 GCGTACGTGGAAGGTCCGTAGCCCTTGACTGCAAGAGTCTGATGAGCTCTC 7980
QY 7978 TGCAGATCAAGTACT 7992
Db 7981 TGCAGATCAAGTACT 7995

RESULT 14
AAA98967
ID AAA98967 standard; DNA; 8001 bp.
XX
AC AAA98967;
XX
DT 08-FEB-2001 (first entry)
DE
XX Hepatitis C virus DNA fragment SEQ ID NO: 3.
XX
KW Cell culture; therapy; infection; vaccine; diagnosis; gene therapy; ds.
XX
OS Hepatitis C virus.
XX
PN DE19915178-A1.
XX
PD 05-OCT-2000.
XX
PF 03-APR-1999; 99DE-1015176.
XX
PR 03-APR-1999; 99DE-1015178.
XX
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX
PI Bartschlagel R;
XX
DR WPI; 2000-629140/61.
XX
PT Cell culture system for hepatitis C virus, useful e.g. in screening for
PT therapeutic agents, comprises human hepatoma cells containing a viral
PT RNA construct that includes a selectable gene -
XX
PS Claim 7: Page 30-36; 58pp; German.
XX
CC This invention describes a novel Hepatitis C virus (HCV) cell culture
CC system comprising human hepatoma cells that contain an integrated HCV-RNA
CC construct (I). (I) contains the HCV-specific RNA segments 5'-NTR
CC (non-translated region), NS (non-structural)1,3, NS4A, NS4B, NS5A, NS5B and
CC 3'-NTR, and a selectable (marker) gene (II). The cell cultures, and/or
CC (I), are used to prepare, evaluate and/or test therapeutic and/or
CC diagnostic agents for HCV infections, and to prepare vaccines against HCV
CC infection (particularly preparation of attenuated HCV). The can also be
CC used for preparation of a liver-specific delivery system for gene
CC therapy, and to identify cells permissive for HCV replication. Virus RNA
CC replicates autonomously and with high efficiency in this cellular system,
CC so that variations in replication rates can be measured (for screening

CC antiviral agents) quantitatively or qualitatively, using standard
 CC laboratory equipment. Efficient replication of HCV RNA is only achieved
 CC when the specified RNA segments are present and when the transfected
 CC cells are maintained under permanent selection pressure.
 XX

Sequence 8001 BP; 1652 A; 2373 C; 2244 G; 1732 T; 0 other:

Query Match 99.68; Score 7960.6; DB 21; Length 8001;

Best Local Similarity 99.88; Pred. No. 0; Mismatches 4; Indels 12; Gaps 1;

QY	1	GCCAGCCCCGATTTGGGGGCGACACTCCACCATATGATCTCCCTGTGAGAACTACTG	60
DB	1	GCCAGCCCCGATTTGGGGGCGACACTCCACCATATGATCTCCCTGTGAGAACTACTG	60
QY	61	TCTTACCCGAGAAAGCGCTAGCATGGCGTTAGTATGATGTGTGGACACCTCCAGGAC	120
DB	61	TCTTACCCGAGAAAGCGCTAGCATGGCGTTAGTATGATGTGTGGACACCTCCAGGAC	120
QY	121	CCCCCTCCCGGAGAGCCATATGTGTGTGGGAAACCGGTGAGTACACCGGAATTGCCAG	180
DB	121	CCCCCTCCCGGAGAGCCATATGTGTGTGGGAAACCGGTGAGTACACCGGAATTGCCAG	180
QY	181	GACGACGGGTCTCTTCTTGGATCAACCCGCTCATGCTCCGAGATTGGGGCTGCCCCC	240
DB	181	GACGACGGGTCTCTTCTTGGATCAACCCGCTCATGCTCCGAGATTGGGGCTGCCCCC	240
QY	241	GCGAGACTGCTAGCCGATAGTGTGGGTGCGGAAAGCCCTTGTGACTGCTGATAGG	300
DB	241	GCGAGACTGCTAGCCGATAGTGTGGGTGCGGAAAGCCCTTGTGACTGCTGATAGG	300
QY	301	GTGCTGTGAGTGGCCCGGAGGTCTGTGTAACCTGACCATGAGACAGAACTCTTAAC	360
DB	301	GTGCTGTGAGTGGCCCGGAGGTCTGTGTAACCTGACCATGAGACAGAACTCTTAAC	360
QY	361	CTCAAGAGAAAAACCAA-----GAGCGCGCATGATTTGAACAAGATGATGCTC	408
DB	361	CTCAAGAGAAAAACCAAAGTACACAAAGGGCGCGCATGATTTGAACAAGATGATGCTC	420
QY	409	ACGAGGTTTCCCGCGGCTTGGGTGAGAGAGCTATTCGCTATGATGGGCAACAACA	468
DB	421	ACGAGGTTTCCCGCGGCTTGGGTGAGAGAGCTATTCGCTATGATGGGCAACAACA	480
QY	469	CAATGGCTGCTGATGACCCGCTGTTCGCGGTGTGACGAGGCGCGCGCTCTTT	528
DB	481	CAATGGCTGCTGATGACCCGCTGTTCGCGGTGTGACGAGGCGCGCGCTCTTT	540
QY	529	TTGTCAACACCGACTGTCCGCTGCTGATGAATGACTGCAAGAGAGCGCGGCTAT	588
DB	541	TTGTCAACACCGACTGTCCGCTGCTGATGAATGACTGCAAGAGAGCGCGGCTAT	600
QY	589	CGTGGCTGGCAGACGAGGCGCTTCTTGGCGAGCTGTGCTGAGCGTTGTACTGAGCGG	648
DB	601	CGTGGCTGGCAGACGAGGCGCTTCTTGGCGAGCTGTGCTGAGCGTTGTACTGAGCGG	660
QY	649	GAGGAGCTGCTGCTATTTGGGCGAAGTGCAGGGGCGAGGATCTCTGTCTATCTCACCTTG	708
DB	661	GAGGAGCTGCTGCTATTTGGGCGAAGTGCAGGGGCGAGGATCTCTGTCTATCTCACCTTG	720
QY	709	CTCCGCGGAGAAAGTATCATATGCTGATGCAATGCGGGGCTGCAATACCTTGATC	768
DB	721	CTCCGCGGAGAAAGTATCATATGCTGATGCAATGCGGGGCTGCAATACCTTGATC	780
QY	769	CGGCTACCTGCCATTGACCAACCAAGCAATGCAATGCAAGCAGCAGTACTCGGA	828
DB	781	CGGCTACCTGCCATTGACCAACCAAGCAATGCAATGCAAGCAGCAGTACTCGGA	840
QY	829	TGGAAGCGGCTGTGTGATGAGATGATGAGACGAAGAGCATCAAGGGGCTGGCCGAG	888
DB	841	TGGAAGCGGCTGTGTGATGAGATGATGAGACGAAGAGCATCAAGGGGCTGGCCGAG	900
QY	889	CCGAACCTTTCGACAGGCTCAAGCGGCGCATGCCGAGCGGAGGATCTCTGTGATGCC	948

DB	901	CCGACCTGTGGCCAGGCTCAAGGCGCGCATGCCCGGCGAGAGATCTCTGTGATGCC	960
QY	949	ATGGCGATGCTGCTGCTGCCGAATATCATGTGTGAAAAATGGCGCTTTTGTGATTCATG	1008
DB	961	ATGGCGATGCTGCTGCTGCCGAATATCATGTGTGAAAAATGGCGCTTTTGTGATTCATG	1020
QY	1009	ACTGTGGCGGCTGCTGCTGCGGAGCGCTATCAGACATAGCGTGGCTACCCGATATA	1068
DB	1021	ACTGTGGCGGCTGCTGCTGCGGAGCGCTATCAGACATAGCGTGGCTACCCGATATA	1080
QY	1069	TTGCTGAAGACTTGGCGGGAATGAGCTACCGCTTCTCTGCTTTACGGATATCGCG	1128
DB	1081	TTGCTGAAGACTTGGCGGGAATGAGCTACCGCTTCTCTGCTTTACGGATATCGCGG	1140
QY	1129	CTCCGATTCGACGCGATGCGCTTCTATGCGCTTGTGAGAGTCTTCTGAGTTTAA	1188
DB	1141	CTCCGATTCGACGCGATGCGCTTCTATGCGCTTGTGAGAGTCTTCTGAGTTTAA	1200
QY	1189	CAGACACACAGCTTCTCTTACGCGGATCAATTCGCGCCCTCTCCCTCCCCCCT	1248
DB	1201	CAGACACACAGCTTCTCTTACGCGGATCAATTCGCGCCCTCTCCCTCCCCCCT	1260
QY	1249	AACGTTACTGGCGAGACCGCTTGGAAATAGGCGCGGTGCTGCTGATATGATTT	1308
DB	1261	AACGTTACTGGCGAGACCGCTTGGAAATAGGCGCGGTGCTGCTGATATGATTT	1320
QY	1309	TCACACATATTCGCTTTTGGCAATGTAGGAGCGCGGAAACCTGCTCTTCTTG	1368
DB	1321	TCACACATATTCGCTTTTGGCAATGTAGGAGCGCGGAAACCTGCTCTTCTTG	1380
QY	1369	ACGAGCATTCCTAGGGGCTTTTCCCTCTGCGCAAGAAATGGAAGTCTGTTGAATGTC	1428
DB	1381	ACGAGCATTCCTAGGGGCTTTTCCCTCTGCGCAAGAAATGGAAGTCTGTTGAATGTC	1440
QY	1429	GTGAAGAGAGTCTCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTAGGACCTT	1488
DB	1441	GTGAAGAGAGTCTCTCTGGAAGCTTCTTGAAGCAAAACAGCTGTAGGACCTT	1500
QY	1489	TGCAAGCGAGGAAACCCCGACCTGGGAGAGAGTGCCTGCGGCAAAAGCAGCTGTA	1548
DB	1501	TGCAAGCGAGGAAACCCCGACCTGGGAGAGAGTGCCTGCGGCAAAAGCAGCTGTA	1560
QY	1549	TAAATACACCTGCAAGAGCGGAGCAACCCAGTGCAGCTTGTGATGATGTTG	1608
DB	1561	TAAATACACCTGCAAGAGCGGAGCAACCCAGTGCAGCTTGTGATGATGTTG	1620
QY	1609	GAAAGAGTCAAATGGCTCTCTCAAGGATTTCAACAAGGGGCTGAAGATGCCCAAG	1668
DB	1621	GAAAGAGTCAAATGGCTCTCTCAAGGATTTCAACAAGGGGCTGAAGATGCCCAAG	1680
QY	1669	GTACCCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1728
DB	1681	GTACCCCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1740
QY	1729	TCGAGGTTAAAAAGCTCTGAGCGCCCGGACCAAGCGGAGCGTGTGTTTCTTTGAAAA	1788
DB	1741	TCGAGGTTAAAAAGCTCTGAGCGCCCGGACCAAGCGGAGCGTGTGTTTCTTTGAAAA	1800
QY	1789	CACGATATACATGAGCGGCTATTAAGGCTTATCCCAACAGAGCGGAGGCTTATGAC	1848
DB	1801	CACGATATACATGAGCGGCTATTAAGGCTTATCCCAACAGAGCGGAGGCTTATGAC	1860
QY	1849	TGCATCATCTAGCTCTACAGGCGGAGACAGGACAGGTCGAGGAGGCTCAGGTG	1908
DB	1861	TGCATCATCTAGCTCTACAGGCGGAGACAGGACAGGTCGAGGAGGCTCAGGTG	1920
QY	1909	GTCTCCACCGGAACACATTTTCTCTGCGCACCTGCGTCAATGAGGCTGTGAGACTGTC	1968
DB	1921	GTCTCCACCGGAACACATTTTCTCTGCGCACCTGCGTCAATGAGGCTGTGAGACTGTC	1980
QY	1969	TATCATGCTGCGGCTCAAGAGCCCTTGCAGGCGCAAGGGCCCAATCAACCAATGATC	2028
DB	1981	TATCATGCTGCGGCTCAAGAGCCCTTGCAGGCGCAAGGGCCCAATCAACCAATGATC	2040

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QY 2029 ACCAATGTGACACGAGACCTGTGCGCTGGCAAGCGCCCCCGGGGCGCTTCTTGACA 2088
DB 2041 ACCAATGTGACACGAGACCTGTGCGCTGGCAAGCGCCCCCGGGGCGCTTCTTGACA 2100
QY 2089 CCATACCACTGCGGAGAGTGTGACCTTACTGTGTACAGAGCATGCGATGTGATTCGCG 2148
DB 2101 CCATACCACTGCGGAGAGTGTGACCTTACTGTGTACAGAGCATGCGATGTGATTCGCG 2160
QY 2149 GTGCGCGCGGCGGCGGACAGCAGGAGGAGACCTTACTGTGTGCGGAGCGCGGTCTTACTG 2208
DB 2161 GTGCGCGCGGCGGCGGAGCAGCAGGAGGAGCCTTACTGTGTGCGGAGCGCGGTCTTACTG 2220
QY 2209 AAGGGCTCTTGGGGGGGTGCACAGCTGTGCGGCGGAGCAGCTGTGGGCACTTTCG 2268
DB 2221 AAGGGCTCTTGGGGGGGTGCACAGCTGTGCGGCGGAGCAGCTGTGGGCACTTTCG 2280
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QY 2329 GAAACCACTATACCGGCTCCCGGCTCTTCACGAGCACTGTGCGGCGGCTACCGGAG 2388
DB 2341 GAAACCACTATACCGGCTCCCGGCTCTTCACGAGCACTGTGCGGCGGCTACCGGAG 2400
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DB 2401 ACATTCCAGGTGGCCCATCTACAGCGCCCTACTGTGTAGCGGCAAGAGCACTAAGTCCG 2460
QY 2449 GCTGCGTATGACGCCCAAGGAGTATAGGTGCTTGTCTGGAACCGGTCCGTGCGGCGCAC 2508
DB 2461 GCTGCGTATGACGCCCAAGGAGTATAGGTGCTTGTCTGGAACCGGTCCGTGCGGCGCAC 2520
QY 2509 CTAGGTTTGGGGGCTATATGTCTAAGGACATGGTATGACGCCCTAACATCAGAACCGG 2568
DB 2521 CTAGGTTTGGGGGCTATATGTCTAAGGACATGGTATGACGCCCTAACATCAGAACCGG 2580
QY 2569 GTAAGAGCACTATACCAAGGAGTCCCGCATCAGTACTCCACCTATGGCAATTTCTTGCC 2628
DB 2581 GTAAGAGCACTATACCAAGGAGTCCCGCATCAGTACTCCACCTATGGCAATTTCTTGCC 2640
QY 2629 GAGGAGTGTGCTGCGGAGGCGCTATGACATCATATATGTGATGATGCTGCTCACT 2688
DB 2641 GAGGAGTGTGCTGCGGAGGCGCTATGACATCATATATGTGATGATGCTGCTCACT 2700
QY 2689 GACTGACCACTATCTGTGGGCAATGCGCACAGTCTGTGACCAAGCGGAGCGGTGAGCG 2748
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DB 2821 ATGAGAGAGTGTGCTGTCCAGCACTGAGAAATCCCTTTTATGCAAAAGCCATCCG 2880
QY 2869 ATGAGAGCACTAAGGAGGAGGAGGAGCACTATTTTCTGCAATTCAGAAAGAAATGTGAT 2928
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DB 3001 GATGTATCCGTATACCAACTAGCGAGAGCTGATGTGTGAGCAAGCGAGCTGTATG 3060
QY 3049 ACGGGCTTTACGGGAGATTTGAGTACAGTACGAGTCAATATACATGTGTACCCAGCA 3108
DB 3061 ACGGGCTTTACGGGAGATTTGAGTACAGTACGAGTCAATATACATGTGTACCCAGCA 3120

QY 3109 GTGCACTTCAGGCTGAGACCGGACCTTCACCATGTAGAGAGAGAGACCGGTGCCAAGAGCGG 3168
DB 3121 GTGCACTTCAGGCTGAGACCGGACCTTCACCATGTAGAGAGAGAGACCGGTGCCAAGAGCGG 3180
QY 3169 GTGTACGCTGAGAGCGGCGAGGAGAGAGTGTGTAGGAGGAGAGATGGGCATTTACAGGTTT 3228
DB 3181 GTGTACGCTGAGAGCGGCGAGGAGAGAGTGTGTAGGAGGAGAGATGGGCATTTACAGGTTT 3240
QY 3229 GTGATCCAGAGAGAGCGGCGGCGGAGTGTGTATGATTCCTCGGTTGTGTGCGAGTGTAT 3288
DB 3241 GTGATCCAGAGAGAGCGGCGGCGGAGTGTGTATGATTCCTCGGTTGTGTGCGAGTGTAT 3300
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DB 3301 GAGCGGCGCTGTGTTGTGTAGAGCTACGCGCGCGAGACCTTGTAGGTTGCGGCT 3360
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DB 3361 TACCTAAACACACAGGAGTTCGCGCTGTGCGAGACCATCTGGAGTCTGGGAGAGCTC 3420
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DB 3421 TTTACAGGCTTCACCCACATAGAGCGCCATTTCTTGTCCAGACTAAGAGAGAGAGAC 3480
QY 3469 AACTTCCCTTACTGTGTGTAGCATACAGGCTACGCTGTGCGGAGGCTCAGGCTCCACT 3528
DB 3481 AACTTCCCTTACTGTGTGTAGCATACAGGCTACGCTGTGCGGAGGCTCAGGCTCCACT 3540
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DB 3541 CCATGCGGAGCAATGTGAGAGTGTCTCATAGCGGCTAAAGCTACGCTGACAGGAGCA 3600
QY 3589 ACGCCCTGCTGTATAGGCTGAGAGCGCTTCAAAAGAGGTTACTACACACACCCATA 3648
DB 3601 ACGCCCTGCTGTATAGGCTGAGAGCGCTTCAAAAGAGGTTACTACACACACCCATA 3660
QY 3649 ACCAATATCATGTGAGCATGTGCGGCTACCGGAGGCTGACAGAGACCTGAGTG 3708
DB 3661 ACCAATATCATGTGAGCATGTGCGGCTACCGGAGGCTGACAGAGACCTGAGTG 3720
QY 3709 CTGCTAGGCGGAGTCTGTAGCACTGTGCGCGGCTATTGCTCTGACACAGGCGGTGCTC 3768
DB 3721 CTGCTAGGCGGAGTCTGTAGCACTGTGCGCGGCTATTGCTCTGACACAGGCGGTGCTC 3780
QY 3769 ATTGTGAGAGATCATCTGTGCGGAGAGCGCGCATCATTTCCGAGAGGAGTCTT 3828
DB 3781 ATTGTGAGAGATCATCTGTGCGGAGAGCGCGCATCATTTCCGAGAGGAGTCTT 3840
QY 3829 TACCGGAGTGTGATGAGTGAAGAGTGCCTACACCTCCCTTACATGAGAACAGGA 3888
DB 3841 TACCGGAGTGTGATGAGTGAAGAGTGCCTACACCTCCCTTACATGAGAACAGGA 3900
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QY 3949 CAAGCGAGAGTGTGCTGCTGCGGCTGTGGAATCAAGTGGCGAGACCTGGAAGCTTCTG 4008
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 Db 7981 TGGCCTCTGTGCAGATCAAGT 8001

RESULT 15
 AAD25323
 ID AAD25323 standard; CDNA; 7848 BP.
 AC AAD25323:
 DT 12-MAR-2002 (first entry)
 DE Hepatitis C virus (HCV) adaptive replicon I CDNA mutant.
 KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
 adaptive replicon I; mutant; ss.
 OS Hepatitis C virus.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH 4642..5841
 FT CDS
 FT /*lag- a
 FT /*product= "NS5A protein of HCV adaptive replicon I"
 FT /note= "CDS does not include both start and stop
 codon"
 FT /partial
 EN W0200189364-A2.
 PD 29-NOV-2001.
 PF 23-MAY-2001; 2001WO-US16822.
 PR 23-MAY-2000; 2000US-0576989.
 PA (UNIW) UNIV WASHINGTON.
 PI Rice CM, Blight RJ;

XX WPI: 2002-066755/09.
DR P-PSDB: AAE15719.
XX
XX Hepatitis C virus variants having greater transfection efficiency and
PT ability to survive subpassage, useful as a vaccine for immunizing
PT primate to the virus, comprise non-naturally occurring viral sequences
XX
PS Claim 17, Page 72-74; 174pp; English.

XX The invention relates to Hepatitis C virus (HCV) variants which include
CC polynucleotides comprising non-naturally occurring HCV sequence and HCV
CC variants that have a transfection efficiency and ability to survive
CC subpassage greater than HCV that have wild-type polypeptide coding
CC regions. The polynucleotides of the invention are useful for identifying
CC a cell line that is permissive for infection with HCV and detecting
CC replication of HCV in cells of the cell line. They are also useful for
CC testing a compound for anti-viral properties and for inhibiting HCV
CC infection. They are also useful for the generation of defined HCV virus
CC stocks to develop in vitro and in vivo assays for virus neutralisation,
CC attachment, penetration and entry, structure/function studies on HCV
CC proteins and RNA elements and identification of new antiviral targets,
CC a systematic survey of cell culture systems and conditions to identify
CC those that support wild-type and variant HCV RNA replication and
CC particle release, production of adaptive HCV variants capable of more
CC efficiency replication in cell culture, production of HCV variants with
CC altered tissue or species tropism, establishment of alternative animal
CC models for inhibitor evaluation including those supporting HCV variant
CC replication, development of cell-free HCV replication assays,
CC production of immunogenic HCV particles for vaccination, engineering of
CC attenuated or defective HCV derivatives for expression of
CC heterologous gene products for gene therapy and vaccine applications
CC and for utilisation of the HCV glycoproteins for targeted delivery of
CC therapeutic agents to the liver or other cell types with appropriate
CC receptors. Vaccine comprising these sequences is useful for inducing
CC immunoprotection to HCV in a primate. The present sequence is
CC Hepatitis C virus (HCV) adaptive replicon 1 cDNA mutant. This sequence
CC is generated by the deletion of nt 5345-5485 of HCVrepBattman/Avair
CC cDNA.
XX
XX
SQ Sequence 7848 BP; 1614 A; 2328 C; 2202 G; 1704 T; 0 other;

Query Match 96.2%; Score 7689; DB 24; Length 7848;
Best Local Similarity 98.2%; Pred. No. 0;

Matches 7843; Conservative 0; Mismatches 5; Indels 141; Gaps 1;

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DB 1 GCCAGCCCCCGATTGGGGGCGACACTCCACCATAGATACCTCCCTGTGAGGAATCTAGT 60
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DB 61 TCTTCACGAGAAGCGGTATGCGTGGGTAGTATGATGCTGCGAGCGCTCCAGAC 120
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DB 121 CCCCCCTCCCGGAGACCATAGTGTCTGCGAAACCGGTAGTACACCGGAATTGGCAG 180
QY 181 GAGGACGGGGTCTTCTTGATCAACCGGCTCATGCTGAGATTGGGCGTGGCCCC 240
DB 181 GAGGACGGGGTCTTCTTGATCAACCGGCTCATGCTGAGATTGGGCGTGGCCCC 240
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DB 541 ACCTGTCCGGTCCCTGATGACGAGACGAGGCGGCTATGCTGCTGCGCA 600
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DB 661 TGCTATTGGGGGAAGTGGCGGGGAGAGATCTCTGTCATCTACCTTGTCTGCGAGA 720
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DB 841 TTGTGATCAGGATATGTGACGAGAGCATGAGGGGCTGCGCCAGCGAAGTGTTCG 900
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QY 961 GCTTCCGCAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
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QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAGTGTGAGGACCTTGTGAGGACGCG 1500
DB 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAGTGTGAGGACCTTGTGAGGACGCG 1500

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Db	1441	GTCTCTGAGACTTCTTGAAAGCAAAACAAGCTGTGTAAGGACCCCTTTCAGGACACGG	1500
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Db	1501	AACCCCCACCTGGCGACAGAGTGCCTCTGCGGCCAAAGACCAAGCTGTATTAAGATACACT	1560
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Db	1561	GCAAGGCGGACACACCCCAAGTCCACAGTGTGAGTGGATAGTGTGGAAGAAGGTCAA	1620
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Db	1621	TGGCTCTCTCAACCTATTCACACAAGAGGGCTGAAGAGATAGCCCAAGATGCCCATGT	1680
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Qy	2281	ACCCGAGGGGTTGGAAAGGGGTGGAATTTGTACCCGCTGAGAGCTATGGAACCACTATG	2340
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Qy	2341	CGGTCCCGGCTTTCACAGCAACTCTTCCCTCCGCGCGTACCGCAGACATTTCCAGGTG	2400
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Qy	2461	GCCCAAGGTTAAGTGTCTGTCTTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG	2520
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Qy	2521	GCGTATATGTCTAAGGACATGTGATGACCCCTAACATCAGAACCGGGGTAAAGACATC	2580
Db	2521	GCGTATATGTCTAAGGACATGTGATGACCCCTAACATCAGAACCGGGGTAAAGACATC	2580

QY	2591	ACCAAGGGTGGCCCCATACAGTACTCCACTATGGCAGATTCTCTGGCCGAGCGTGGTGC	2640
Db	2591	ACCAAGGGTGGCCCCATACAGTACTCCACTATGGCAGATTCTCTGGCCGAGCGTGGTGC	2640
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Db	2641	TCCTGGGGGGCGCTATGATCATCATATATATGATGATGATGTCACCTCACTCACTCGACCACT	2700
QY	2701	ATCTCGGGCATCGGCACACAGTCTCGACCAAGGGGAGACGGCTGGAGGCCCACTGTGGTG	2760
Db	2701	ATCTCGGGCATCGGCACACAGTCTCGACCAAGGGGAGACGGCTGGAGGCCCACTGTGGTG	2760
QY	2761	CTCGGCAACCGGTAGCGCTCCGGGATGGTGCACCGTCCCATCCAAACATGAGAGAGTG	2820
Db	2761	CTCGGCAACCGGTAGCGCTCCGGGATGGTGCACCGTCCCATCCAAACATGAGAGAGTG	2820
QY	2821	GCTCTGTCCAGCACTGGAAGAAATCCCTTTTATAGCAAGGCATCCCATCGAGACCATC	2880
Db	2821	GCTCTGTCCAGCACTGGAAGAAATCCCTTTTATAGCAAGGCATCCCATCGAGACCATC	2880
QY	2881	AAGGGGGGAGAGCACTCATTTTCTGCATCCCAACAAATAATGATGAGCTGGCGCG	2940
Db	2881	AAGGGGGGAGAGCACTCATTTTCTGCATCCCAACAAATAATGATGAGCTGGCGCG	2940
QY	2941	AAGCTGTCCGGCTCTCGGACATCATGCTGTATGCAATTACGGGGGCTTGATGTCCGTG	3000
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QY	3601	TATAGCTGGAGCGCGTTCAAAACAGAGTTACTACACACACCCCATTAACCAATATCATC	3660
Db	3601	TATAGCTGGAGCGCGTTCAAAACAGAGTTACTACACACACCCCATTAACCAATATCATC	3660


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Mon Jun 2 08:44:24 2003

us-10-005-469-4.rng

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Search completed: May 31, 2003, 05:02:36
Job time : 1019 secs

Mon Jun 2 08:44:25 2003

us-10-005-469-4.rn1

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GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 30, 2003, 20:03:05 ; Search time 153 Seconds
(without alignments)
16019.351 Million cell updates/sec

Title: US-10-005-469-4

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5218	65.3	7917	1	US-08-324-977-31
3	5218	65.3	7917	2	US-08-384-616-31
4	5218	65.3	7917	2	US-08-904-686A-31
5	5218	65.3	7917	4	US-09-315-850-31
6	5218	65.3	9416	1	US-08-324-977-1
7	5218	65.3	9416	2	US-08-384-616-1
8	5218	65.3	9416	2	US-08-904-686A-1
9	5218	65.3	9416	4	US-09-315-850-1
10	5175.2	64.8	7863	1	US-08-823-895A-27
11	5175.2	64.8	7863	1	US-08-324-977-35
12	5175.2	64.8	7863	2	US-08-384-616-35
13	5175.2	64.8	7863	2	US-08-904-686A-35
14	5175.2	64.8	7863	4	US-09-315-850-35
15	5175.2	64.8	9030	1	US-08-324-977-13
16	5175.2	64.8	9030	2	US-08-384-616-13
17	5175.2	64.8	9030	2	US-08-904-686A-13
18	5175.2	64.8	9030	4	US-09-315-850-13
19	4100.6	51.3	9599	3	US-09-014-416-2
20	4099	51.3	9599	3	US-09-014-416-6
21	4094.6	51.2	9646	3	US-08-811-566-1
22	4094.6	51.2	9646	4	US-09-034-756-1
23	4091	51.2	12980	4	US-08-811-566-5
24	4091	51.2	12980	4	US-09-034-756-5
25	4018.2	50.3	9379	4	US-09-388-874-1
26	4018.2	50.3	9401	1	US-07-910-760-9
27	4018.2	50.3	9401	1	US-08-440-519-9

28	4018.2	50.3	9401	4	US-08-440-549-9	Sequence 9, Appl1
29	4018.2	50.3	9401	4	US-08-823-895A-25	Sequence 25, Appl1
30	4017.4	50.3	9401	5	PCT-US91-02225-9	Sequence 9, Appl1
31	4016.2	50.3	9379	3	US-08-444-818-176	Sequence 176, Appl
32	3967.2	49.6	9416	4	US-08-811-566-19	Sequence 19, Appl
33	3967.2	49.6	9416	4	US-09-034-756-19	Sequence 19, Appl
34	3962.8	49.6	8987	4	US-08-444-818-137	Sequence 137, Appl
35	3959	49.5	9401	2	US-08-432-693-1	Sequence 1, Appl1
36	3941.6	49.3	9416	4	US-08-823-895A-26	Sequence 26, Appl
37	3879.6	48.5	9185	3	US-08-444-818-122	Sequence 122, Appl
38	3879.6	48.5	9185	3	US-08-444-818-123	Sequence 123, Appl
39	3710	46.4	6785	3	US-08-444-818-65	Sequence 65, Appl
40	3710	46.4	7310	3	US-08-444-818-74	Sequence 74, Appl
41	3710	46.4	8316	3	US-08-444-818-88	Sequence 88, Appl
42	3289.8	41.2	3750	4	US-08-191-160-22	Sequence 22, Appl
43	2781.6	35.9	5360	3	US-08-444-818-53	Sequence 53, Appl
44	2781.6	34.8	9589	1	US-07-925-695-1	Sequence 1, Appl1
45	2781.6	34.8	9589	1	US-07-925-695-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1	
US-09-014-416-4	Sequence 4, Application US/09014416
Patent No. 6153421	
GENERAL INFORMATION:	
APPLICANT: Yanaqil, Masayuki	
APPLICANT: Bukh, Jens	
APPLICANT: Emerson, Susanne U.	
APPLICANT: Purcell, Robert H.	
TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND	
FILE REFERENCE: 20264276	
CURRENT APPLICATION NUMBER: US/09/014,416	
CURRENT FILING DATE: 1998-01-27	
EARLIER APPLICATION NUMBER: US 60/053,062	
EARLIER FILING DATE: 1997-07-18	
NUMBER OF SEQ ID NOS: 65	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 4	
LENGTH: 9595	
TYPE: DNA	
ORGANISM: Hepatitis C virus	
US-09-014-416-4	
Query Match	66.5%; Score 5312; DB 3; Length 9595;
Best Local Similarity	91.3%; Pred. No. 0;
Matches 5650; Conservative	0; Mismatches 530; Indels 10; Gaps 1;
1800	CATGGGCGCTATTAGCGCTACTCCACAGAGCGGAGGCGCTACTGGCTGCATCATCAC 1859
3416	CCTGGGCGCATACGCGCTACTCCACAGAGCGGAGGCGCTACTGGCTGCATCATCAC 3475
1860	TACCCCTACAGGCGCGGACAGAGAGGAGGAGGTCCAGTGGTCTCCACGCG 1919
3476	TACCCCTACAGGCGCGGACAGAGAGGAGGAGGTCCAGTGGTCTCCACGCG 3535
1920	AACACATCTTCTCTGCGGACCTGGCTAATGCGCTGTGAGTCTCTATCATGAGC 1979
3536	AACACATCTTCTCTGCGGACCTGGCTAATGCGCTGTGAGTCTCTATCATGAGC 3595
1980	CGGCTAAAGACCTTCCGCGGCGCAAGGCGCAATACCAATGTACCAATGTAGA 2039
3596	TGGCTGAGAGACCTTCCGCGGCGCAAGGCGCAATACCAATGTACCAATGTAGA 3655
2040	CCAGGACCTCTGCGGTGCGCAAGGCGCGCGGCGGCTCTTGAACCATGACCTG 2099
3656	CCAGGACCTCTGCGGTGCGCAAGGCGCGCGGCGGCTCTTGAACCATGACCTG 3715
2100	CGGACCTCTGCGGTGCGTACGAGGAGCATGCGATGATTCGATGCGGCGGCGG 2159

Db 3716 TGCGAGCTCGGACCTTTACTTGGTCAAGAGACATGCTGATGTCATTCGGGTGCGCGCG 3775
Qy 2160 GGGGAGAGAGAGGGAGGCTACTCTCCCCAGGGCCGCTCTCTACTTGAAGGGCTCTC 2219
Db 3776 AGCGAGAGAGAGGGGAAGTCTACTCTCCCCAGGGCCGCTCTCTACTTGAAGGGCTCTC 3835
Qy 2220 GGGGAGTCACTGCTCTGCCCCGCGGGGACAGCTGTGGGCACTCTTTCGGGCTGCGGTG 2279
Db 3836 GGGGTGTCATGCTTGGCCCTTCGGGGACAGCTGTGGGCTCTTTCGGGCTGCGGTG 3895
Qy 2280 CACCCGAGGGGTGGCGAAGGGGTGGACCTTGGACCCGTCGAGTGTATGGAAACACAT 2339
Db 3896 CACCCGAGGGGTGGCGAAGGGGTGGACCTTGGACCCGTCGAGTGTATGGAAACACAT 3955
Qy 2340 GCGGTCCCGCTCTTCAGGACACTGTCCCTCCGCGCTACCGACATTCAGGT 2399
Db 3956 GCGGTCTCGGCTTTCAGACACTCAACCCCCCGGCTGTACCGACATTCAGGT 4015
Qy 2400 GGGCCATCTACAGCCCTCTACTGTAGCGGCAAGAGACTAGTGGCGGCTGCGTATGC 2459
Db 4016 GGGCAATCTGACGCTCTACTGTGACGGCAAGAGACCAAGATGCGGCTGCGTATGC 4075
Qy 2460 AGCCCAAGGGGTATAGGTGCTTGTCTGTAACCCGTCGCGCCACCCATGAGTTGCG 2519
Db 4076 AGCCCAAGGGGTATAGGTGCTTGTCTGTAACCCGTCGCGCCACCCATGAGTTGCG 4135
Qy 2520 GGGCTATATGCTTAAGGACATAGTATCGACCTTACATCAGACCGGGGTAAAGACAT 2579
Db 4136 GGGCTATATGCTTAAGGACATAGTATCGACCTTACATCAGACCGGGGTAAAGACAT 4195
Qy 2580 CACCAAGGGGTGCCCCATCAAGTACTCACTATGCAAGTTTCTTCCGAGCGTGGTTCG 2639
Db 4196 TACCAAGGGGTGCCCCATCAAGTACTCACTATGCAAGTTTCTTCCGAGCGTGGTTCG 4255
Qy 2640 CTCTGGGGGGGCTTATACATCAATATATGTATGATGGCACTTCACTGATCCAGCAC 2699
Db 4256 TTCTGGGGGGGCTTATACATCAATATATGTATGATGGCACTTCACTGATCCAGCAC 4315
Qy 2700 TATCTGGGATCGGACACATCTCTGACACAGCGAGAGCGGCTGAGCGCGATCGTCT 2759
Db 4316 CATCTTGGGATCGGACACATCTCTGACACAGCGAGAGCGGCTGAGCGCGATCGTCT 4375
Qy 2760 GCTGCGCAACCGCTACGCTCCGGGATCGGTCAACCGTCCATCCAAATATGAGAGGT 2819
Db 4376 GCTGCGCAACCGCTACGCTCCGGGATCGGTCAACCGTCCATCCAAATATGAGAGGT 4435
Qy 2820 GGGCTGTGCGACACTGGAGAAATCCCTTTATGGAAAGCCATCCCATCGAGACAT 2879
Db 4436 AGGCTGTGCGACAAATGGAGAGATCCCTCTTATGGAAAGCCATCCCATCGAGACAT 4495
Qy 2880 CAAGGGGGGAGGACCTCATTTTCTGCAATTCGAAGAGAAATGTGATGAGTGGCGC 2939
Db 4496 CAAGGGGGGAGGACCTCATTTTCTGCAATTCGAAGAGAAATGTGATGAGTGGCGC 4555
Qy 2940 GAAGTGTGCGGCTCGAGACATGCTGTAGCAATATTAACGGGGCTTATATCGT 2999
Db 4556 AAAGCTGACAGGCTCGGACATGAACGCTGTAGCAATATTAACGGGGCTTATATCGT 4615
Qy 3000 CATACCAACTAGCGGAGAGCTCATTTGCTAGACACGAGCGCTTATATGACGGGCTTAC 3059
Db 4616 CATACCGGCTATCGGAGAGCTCATTTGCTAGGACACGAGCGCTTATATGACGGGCTTAC 4675
Qy 3060 GCGGATTTGAGTCAAGGATCGACTGATACATGATGTAACCCAGAGTCACTTAC 3119
Db 4676 CCGGATTTTACATCAGTACGACTGATACATGATGTAACCCAGAGTCACTTAC 4735
Qy 3120 CCGTGAACCGACTTACACATTTGAGACAGACCGGTGCAACAGCGGTGTACGCTC 3179
Db 4736 CTTGATCCACCTTACACATTTGAGAGACAGCGGTGCAACAGCGGTGTACGCTC 4795
Qy 3180 GAGGAGGAGAGAGAGATGATAGGAGAGATGAGGATTTACAGGTTTGTAGTCCAG 3239
Db 4796 GAAAGGAGAGAGATGATAGGAGAGAGGAGGATGAGGATTTGTAGTCCAG 4855

Qy 3240 AGAAGGACCTCGGAGATTTGATTCCTCGGTTCTGTGCAAGTCTATGACGGGCTG 3299
Db 4856 AGAAGGACCTCGGAGATTTGATTCCTCGGTTCTGTGCAAGTCTATGACGGGCTG 4915
Qy 3300 TGCTTGTACAGACTACAGCCCGGAGACCTTCACTTATGATTTGGGGCTTACTTAAAC 3359
Db 4916 TGCTTGTATGACTACAGCCCGGAGACCTTCACTTATGATTTGGGGCTTACTTAAATAC 4975
Qy 3360 ACCAGGATTCGCTGTGACAGACATGTGAGTTCTGGAGAGCTCTTACAGGCT 3419
Db 4976 ACCAGGATTCGCTGTGACAGACATGTGAGTTCTGGAGAGCTCTTACAGGCT 5035
Qy 3420 CACCCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGAGAGACACTTCCCTA 3479
Db 5036 CACCCACATAGATGCCCATTTCTGTCCAGACTAAGCAGGAGAGACACTTCCCTA 5095
Qy 3480 CCGTGTAGCATACAGGCTACGAGTGTGCGCCAGGGCTGAGCTCCACCTCCATGTTGGA 3539
Db 5096 CCGTGTAGCATATCAGGCTACGAGTGTGCGCCAGGGCTGAGCTCCACCTCCATGTTGGA 5155
Qy 3540 CCAATGTGAGAGTGTCTATACGCTTAAAGCTTACGCTGACAGGGCCACAGCCCTGCT 3599
Db 5156 CCAATGTGAGAGTGTCTATACGCTTAAAGCTTACGCTGACAGGGCCACAGCCCTGCT 5215
Qy 3600 GTATAGGCTGGAGCGGTTCAAAACGAGGTACTACACACACCCCATTAACCAATACAT 3659
Db 5216 GTATAGGCTGGAGCGGTTCAAAACGAGGTACTACACACACCCCATTAACCAATACAT 5275
Qy 3660 CATGCAATGATGTGCGCTGACCTGAGAGTCTGACAGACACTGGGTGCTGTAGGCGG 3719
Db 5276 CATGCAATGATGTGCGCTGACCTGAGAGTCTGACAGACACTGGGTGCTGTAGGCGG 5335
Qy 3720 AGTCTGACAGCTGTGCGCGCTATGCTGACCAACAGGACAGCTGTATGTGGCGAG 3779
Db 5336 AGTCTGACAGCTGTGCGCGCTATGCTGACCAACAGGACAGCTGTATGTGGCGAG 5395
Qy 3780 GATCATCTTGTCCGGAAGCGCGCATCATTCGCGACAGGAAATGCTTACCGGAGTT 3839
Db 5396 GATCATCTTGTCCGGAAGCGCGCATCATTCGCGACAGGAAATGCTTACCGGAGTT 5455
Qy 3840 CGATGAGATGAGAGAGTGGGCTCACAGCTCCCTTACATGCAAGAGGAATGACCTGCG 3899
Db 5456 CGATGAGATGAGAGAGTGGGCTCACAGCTCCCTTACATGCAAGAGGAATGACCTGCG 5515
Qy 3900 CGAACAAATCAAAACAGAGGCAATCGGTTGCTGCAAAACGCGCACCAAGCGAGGCG 3959
Db 5516 CGAACAAATCAAAACAGAGGCGCTCGGTTGCTGCAAAACGCGCACCAAGCGAGGCG 5575
Qy 3960 TGTGCTCGCGGTGGAATCCAAAGTGGGAGCGCTCGAAGCCCTTGGGGAGAGATAT 4019
Db 5576 TGTGCTCGCGGTGGAATCCAAAGTGGGAGCGCTCGAAGCCCTTGGGGAGAGATAT 5635
Qy 4020 GTGAATTTATCAGCGGAGTACAAATATTAGCAGGCTTGTCACTCTGCTGCAAGCC 4079
Db 5636 GTGAATTTATCAGCGGAGTACAAATATTAGCAGGCTTGTCACTCTGCTGCAAGCC 5695
Qy 4080 CGCATATGATCATGATGATGATTCACAGGCTTATACAGCGGCTTACACAGCCCAACA 4139
Db 5696 CGCATATGATCATGATGATGATTCACAGGCTTATACAGCGGCTTACACAGCCCAACA 5755
Qy 4140 TACCTGCTGTTTACATCTCTGGGGGATGAGTGGCGCCCAACTTGTCTCCAGCGC 4199
Db 5756 CACCTGCTGTTTACATCTCTGGGGGATGAGTGGCGCCCAACTGCTCTCCAGCGC 5815
Qy 4200 TGCTTCTGCTTCTGAGGCGCGGATCGTGTGAGGCGGCTTGGAGAGATAGGCTTGG 4259
Db 5816 TGCTTCTGCTTCTGAGGCGCGGATCGTGTGAGGCGGCTTGGAGAGATAGGCTTGG 5875
Qy 4260 GAAAGTGTGTGATATTTTGGAGAGTATGAGAGAGGGGTGCGAGGCGCTGTGTCG 4319
Db 5876 GAAAGTGTGTGATATTTTGGAGAGTATGAGAGAGGGGTGCGAGGCGCTGTGTCG 5935

QY	4320	CTTAAGGTCATAGGCGGGAGATGGCCCTCCACCGAGAGACCTGGCTAACCACTACCTCCCTGC	4379
Db	5936	CTTTAAAGTATAGGCGGAGAGGTGGCTCCACCGAGAGACCTGGTCAACTTACTCCCTGC	5995
QY	4380	TATCTCTCCCTGGCGCCCTAGTGGTGGGGGTCGTGTGGCAGCGATACTGGCTGGCA	4439
Db	5996	CATCTCTCTCCCTGGCGCCCTAGTGGTGGGGGTCGTGTGGCAGCAATATCTGGCTGGCA	6055
QY	4440	CGTGGGCGCCAGGGGAGGGGGGTGTGGAGGATGTAACCGGGTGAATAGGCTTCGGTGGC	4499
Db	6056	CGTGGCGCCGAGGAGAGGGGGGTGTGCAGTGGAATGAACGGCTGATAGGCTTCGGTGGC	6115
QY	4500	GGGTAAACACGTCCTCCCGACGACTATGTGCTGAGAGCAAGCTGCAGCACGTTGCAC	4559
Db	6116	GGGTAAACACGTCCTCCCTACGACTATGTGCTGAGAGCAAGCTGCAGCACGTTGCAC	6175
QY	4560	TCAATCTCTCTAGCTTACCTTACATCACTAGTGGTGAAGAGGGCTCACAGTGGATCA	4619
Db	6176	TCAATCTCTCTAGCTTACCTTACATCACTAGTGGTGAAGAGGGCTCCACAGTGGATTA	6235
QY	4620	CGAGAGCTGCTCCACGCACTGCTCGGGCTGTGGTAAAGATGTTTGGATTGGATATG	4679
Db	6236	TGAAGATGCTCTACGCCATGCTCCGGCTCGTGGCTAAGAGGATGTTTGGATTGGATATG	6295
QY	4680	CACGGTGTACTGATTTCAAGACCTGGCTCCAGTCCAGAGCTCTGGCGGATTCGGGG	4739
Db	6296	CACGGTGTACTGATTTCAAGACCTGGCTCCAGTCCAGAGCTCTGGCGGATTCGGGG	6355
QY	4740	AGTCCCTTCTTCTCATGTCAACGTGGGTACAAAGGAGTCTGGCGGGGCAAGCACTCAT	4799
Db	6356	AGTCCCTTCTTCTCATGTCCCAAGCGGGTACAAAGGAGTCTGGCGGGGCAAGCACTCAT	6415
QY	4800	GCAAAACCACTGGCCATGTTGAGACACAGATATCAACCGACATGTGAAGAAAAGTTCCATAG	4859
Db	6416	GCAAAACCACTGGCCATGCGGAGACACAGATATCCCGGACATGTGMAAAAAGTTCCATAG	6475
QY	4860	GATCTGGGGCCTTAGGACCTGTATGAACAGTGGCATGAGACATTCCCATTTAAGCGTA	4919
Db	6476	GATGTGTGGGCTTAGAAGCCTGTGACAAACAGTGGACCGGAAGTTCCCATTAAGCGATA	6535
QY	4920	CACACAGGCGCCCGCACAGGCTCCCGCGGCGCAATTTATTTAGGGCGCTGTAGCGGT	4979
Db	6536	CACACAGGAGCTTGCACACACCTCCCGCGGCGCAACTTTTCCAGGGCGCTATGGCGGT	6555
QY	4980	GGCTGCTGAGAGATACGTGGAGTTACGGGGTGGGGATTTCCACTACGTACAGGGCAT	5039
Db	6596	GGCTGCTGAGAGATACGTGGAGTTACGGGGTGGGGATTTCCACTACGTACAGGGCAT	6655
QY	5040	GACACTGACAACTAAAGGCCCGGTAGGTTCCGGGCCCGCAATTTCTTACAGAAAT	5099
Db	6656	GACACTGACAACTAAAGTGGCCATGCCAGGTTCCGGGCCCGCAATTTCTTACAGGAAT	6715
QY	5100	GGATGGGGTGGGTTGCACAGAGTACGCTCCAGCGTGCAAACCCCTCTCTACGGGAGAGT	5159
Db	6716	GGATGGAGTGGGTTGCACAGGTACGCTCCGGGTGCAAACCTCTTCTACGGGAGAGT	6775
QY	5160	CACATTCCTGGTGGGCTCATCAATACCTGTGTGGGTACAGCTCCCATGGAGCCGA	5219
Db	6776	CAGTTCACAGGTGGGCTCAACCAATATTTGGTGGGTGCAGCTCCCATGGAGCCGA	6835
QY	5220	ACCGAGAGTACAGTGTCTCACTTCTCATGCTCACCGACCCCTCCACATTTAGGGCGAGAC	5279
Db	6836	ACCGAGAGTACAGTGTCTCACTTCTCATGCTCACCGATCCCTCCACATTTAGCGAGAAC	6895
QY	5280	GGCTAAGCGTAGCTGTGACCGAGGAGTCCGCCCTCTTGGCACCTATCAGTAGCCA	5339
Db	6896	GGCTAAGCGTAGCTGTGACCGAGGAGTCCGCCCTCTTAGCACGTCATCAGTAGCCA	6955
QY	5340	GCTGTCTGGGCTTCTTGAAGGCAACATGACATACCGCTCATGACTCCCGAGAGCTGA	5399
Db	6956	GTTGTCTGGGCTTCTTGAAGGCGAATGACATACCCACACATGATCCCGGAGGCTGA	7015
QY	5400	CGTATCGAGGCCAAGCTCTGTGGCGGACAGAGATGGGCGGGGAAATCACCCCGTTGA	5459

Db	7016	CTCTCATCGAGCCCAACCTCTTGTCGCGGACAGAGATGGGGGAAACATCATCTACCTCGCGTGCA	7075
Qy	5460	GTCCAGAAATTAAGTATGTAATTTTGGACTCTTTTGAGCCCTTCCAAAGGSGAGAGATGA	5519
Db	7076	GTACGAGAAATTAAGTATGTAATTTCTGGACTCTTTTGAAACCGCTTACAGCGGAGGGAGATGA	7135
Qy	5520	GAGGGAAGTATTCGTTCCGGGAGATCTTCGGAGGTCCGAGAAATTTCCCTCGACCAT	5579
Db	7136	GAGGAGATATTCGTTCCGGGAGAGATCTTCGAAATCCAGAAATGTTCCCTCAGCTT	7195
Qy	5580	GCCCATATGSGCACGCCCGGATTTACACCCCTCCACTTTTAGATCTCTGSAAGGACCCGGA	5639
Db	7196	GCCCATATGSGCACGCCCGGATTAACATCCCTCCACTGTAAGATCTCTGSAAGGACCCGGA	7255
Qy	5640	CTACGTCCCTCCAGTGGTACAGGGGTGCATTTCCGCCCTCCGCAAGGCCCTCCGATACC	5699
Db	7256	CTAGTCCCTCCAGTGGTACAGGGATGCCATTTCCACTTCCACTACCAAGGCTCCCTCATACC	7315
Qy	5700	ACCTCCACGAGAGAGAGAGAGGCTGTGTCTCTCTAGAAATCTACCGTCTCTTCGCTTGGC	5759
Db	7316	ACCTCCACGAGAGAGAGAGAGGCTGTGTCTCTCTACGAATCCATATGTCTCTTCCTTGCC	7375
Qy	5760	GGAGCTGGCCACAAACCTTTGGCAGGTCCGATCTCGCCCTCGGCGATGACAGCGCACGGC	5819
Db	7376	GGAGCTGGCCACTAAACCTTTGGTAGTCTCGGATCTCGGCGGTGATAGCGGACGGC	7435
Qy	5820	AAGGACTCTCTCTGACACCAACCTCCGAGAGAGCGGACCGGGATTCGAGACTTGAATCGTA	5879
Db	7436	GACCGCTCTCTCTGACACTTGGCTCCGAGAGAGGTGAACAAAGATTCGAGACTTGAATCGTA	7495
Qy	5880	CTCCTCCATCCCTCCCTTGAAGGGGAGCCCGGGGATCCCGATCTAGGAGAGGGTCTTG	5939
Db	7496	CTCCTCCATCCCTCCCTTGAAGGGGAGCCCGGGGATCCCGATCTAGGAGAGGGTCTTG	7555
Qy	5940	GTCTACCGTAAAGGAGAGGCTATGTGAGAGAGCTGTGTGTGTCCATGTCTCTAACATG	5999
Db	7556	GTCTACCGTAAAGGAGAGGCTATGTGAGAGAGTGTGTGTGTCTCTATGTCTCTATACGTG	7615
Qy	6000	GACAGCGCCCTTATACGCCATCTGCGCTGCGGAGAAACCAAGCTCCCATCAATGCACT	6059
Db	7616	GACAGCGCCCTTATACGCCATCTGCGGCTGCGGAGAAAGTAACTCCCATCAACCGT	7675
Qy	6060	GAGCACTCTTCTGCTCGGACCAACAATGGTGTATGTACCAACATCTCGAGGCGCAG	6119
Db	7676	GAGCACTCTTCTGCTCGGACCAACAATGGTGTATGTACCAACAATCTCCGAGGCGCAG	7735
Qy	6120	CCTCGGACAGAGAGTGTCACCTTTGACAGACTGCAAGTCTGTGAGACCACTACCGGGA	6179
Db	7736	CCTCGGACAGAGAGTGTCACCTTTGACAGATTTGCAAGTCTGTGAGATCATTTACCGGA	7795
Qy	6180	CGTCTCAAGGAGATTAAGGCAAGGCTCCACAGTTAAAGCTTAACCTCTATCCGTGA	6239
Db	7796	CGTCTCAAGGAGATTAAGGCAAGGCTCCACAGTTAAAGCTTATACCTCTATCTATAGA	7855
Qy	6240	GGAAGCTGTAAGCTGAGCGCCCAATTCGCGCAGATCTTAATTTGGCTATGGGCAAA	6299
Db	7856	GGAAGCTGTAAGCTGAGCGCCCAATTCGCGCAAAATTTGGCTATGGGCAAA	7915
Qy	6300	GGAGCTCGGAACTTTCAGAGAAAGCGGTTAACCAATCGGCTCGGTGGAGAGACTT	6359
Db	7916	GGAGCTCGGAACTTTCAGAGAGGCGGTTAACCAATCGGCTCGGTGGAGAGACTT	7975
Qy	6360	GCTGGAAGACTGTAGACACCAATTTGACACCACTATGGAACAAATAATGAGTTTTCTG	6419
Db	7976	GCTGGAAGACTGTAGAACACCAATTTGACACCACTATGGAACAAATAATGAGTTTTCTG	8035
Qy	6420	CGTCCACACGAAAGAGGGGCGGCAACGACGCTCGGCTTATGTATTCAGATTTGGG	6479
Db	8036	CGTCCACACGAAAGAGGGGCGGCAACGACGCTCGGCTTATGTATTCAGACCTGGG	8095
Qy	6480	GGTTCTGTGTGCGAGAAATGGCCCTTACGATGTGTCTCCAGCTCCCTCAGCGCT	6539

D	8096	AGTTCGATGATGAGAGAAAGATGSCCCTTTACGACGAGGCTCCACCCCTTCCTCCAGACCGCT	8153
Q	6540	GATGGGCTCTTATACGAGATCCAAATACCTCTCTGACACGCGGGTCCAGTTCCTGGTGA	6599
D	8156	GATGGGCTCTCTACAGGATTTAAATCTCCCCAAGCAGCGGGTGAGTTCCTGGTGA	8215
Q	6600	TGCCTGGAAGACGAAAGATGCCCTATGSGCTTCGATATGACACCCGCTGTTTGGACTC	6659
D	8216	TACCTGAAATCAAGAAAGATGCCCTATGSGCTTCGATATGACACCCGCTGTTTGGACTC	8275
Q	6660	AACGCTACAGAGATGACATCCGTTGTGAGAGTCAATCTACCAATGTTGACTTGGC	6719
D	8276	AACGCTACAGAGATGACATCCGTTGTGAGAGTCAATCTACCAATGTTGACTTGGC	8335
Q	6720	CCCCAAGCAGACAGCGCCATTAAGTGGCTCAACAGACGCGCTTTACATCGGGGGCCCCCT	6779
D	8336	CCCCAAGCAGCAGACAGCCCAATTAAGTGGCTCAACAGACGCGCTTTACATCGGGGGCCCCCT	8395
Q	6780	GACTAATTTCAAAAGGAGAGACAGTGGGGCTATGCGCGGTGCGCGGAGGGGGTATCTGAC	6839
D	8336	GACTAATTTCAAAAGGAGAGACAGTGGGGCTATGCGCGGTGCGCGGAGGGGGTATCTGAC	8455
Q	6840	GACCACTGCGGGTATACCTCAATGTTACTTGAAGCCGCTCGCGCCTGTGAGCTGC	6899
D	8456	GACTAGCTGGGGTATACCTCAATGTTACTTGAAGCCGCTCGCGCCTGTGAGCTGC	8515
Q	6900	GAACTCTCAGAGACTGCAGATGCTGCTATGCGGAGACAGCTTTCGTTATGTGGAAG	6959
D	8516	AAAGCTCCAGAGACTGCAGATGCTGCTATGCGGAGAGACAGCTTTCGTTATGTGGAAG	8575
Q	6960	CGCGGGACCCCAAGAGACAGACGAGCCTACGCGCCTTACAGAGCCTATGACTAGTA	7019
D	8576	CGCGGGAAACCAAGAGAGATCGGCGGCCCTTACAGAGCCTTACAGAGCCTATGACTAGTA	8635
Q	7020	CTTCGCCCCCTTGGGGACCGCGCCCAACACAGATACGACTTGAAGTTGATTAATCTCATG	7079
D	8636	CTTCGCCCCCTTGGGGATCGGCGGCCCAACACAGATACGAGCTGATTAATCATG	8695
Q	7080	CTCTCTCCAATGTGTACATGCGCGACGATGATCTGGCAAAAGGGTGTACTATCTCACCG	7139
D	8696	TTCTCTCCAATGTGTACATGCGCGACGATGATCTGGCAAAAGGGTGTACTATCTCACCG	8755
Q	7140	TGACCCACACACCCCTCTTGCGGGGCTGGGTGGAGACAGCTAGACACACTCCAGTCAA	7199
D	8756	TGACCCACACACCCCTCTTGCGGGGCTGGGTGGAGACAGCTAGACACACTCCAGTCAA	8815
Q	7200	TTCTCGCTAGGCAACATCATATGATGCGCCCACTTGTGTGGCAAGGATGATCTGAT	7259
D	8816	CTTTGGCTAGGCAATTCATATCATATGATGCGCCCACTTGTGTGGCAAGGATGATCTGAT	8875
Q	7260	GACTCATTTTCTTCCATCCCTTCTAGCTGAGAACACTTGAAGAAAGCCTAGATTGCA	7319
D	8876	GACTCATTTTCTTCCATCCCTTCTAGCTGAGAACACTTGAAGAAAGCCTAGATTGCA	8935
Q	7320	GATCTAGGGGGCCTGTACTCTCATGTAGGCACCTGTAGCTACTCAGATCATTCAGACACT	7379
D	8936	GATCTAGGGGGCCTGTACTCTCATGTAGGCACCTGTAGCTACTCAGATCATTCAGACACT	8995
Q	7380	CCATGAGCCTTAGCGCATTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGAGTGGC	7439
D	8996	CCATGAGCCTTAGCGCATTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGAGTGGC	9055
Q	7440	TTCTATGCTCAGAAATTTGGGGTACCGGCTTGGCAGTCTGTGGAGACATCGGGCCAGAG	7499
D	9056	TTCTATGCTCAGAAATTTGGGGTACCGGCTTGGCAGTCTGTGGAGACATCGGGCCAGAG	9115
Q	7500	TGTCCGCGCTAGGCTACTGTCTCCAGGGGGGAGAGGCTGCCATTTGTGGCAATGACTCTT	7559
D	9116	TGTCCGCGCTAGGCTACTGTCTCCAGGGGGGAGAGGCTGCCATTTGTGGCAATGACTCTT	9155
Q	7560	CAACTGGGCACTAAGACCAAGCTCAAATCACTCAATCCCGGCTGGCTCCCACTTGA	7619
D	9176	TAACTGGGCACTAAGACCAAGCTTAAATCACTCAATCCCGGCGGCTCCCACTTGA	9235

QY	7620	TTTATCCAGGCGTGGTTCCTTCCTGTTACACCGGGGAGACATATATACAGCGCTCTCG	7679
Dd	9236	CTTGCTTGCGTGGTGTCTCCCTGCTTACACCGGGGAGACATATATACAGCGCTCTCG	9295
QY	7680	TGCCGACCGCGCGTGATCATGTGAGTCCCTACTCCACTTTCGTAGGGGTAGGCATCTA	7739
Dd	9296	TGCCGACCGCGCGTGATTCGGTTGCGCTACTCCACTTTCGTAGGGGTAGGCATTTA	9355
QY	7740	TCTACTCCCAACCGATGAACGGGGAGCTACACCTCCAGGCCAATAGGCCATCCTGTT	7799
Dd	9356	CCTCCTCCCAACCGATGAACGGGGAGCTACACCTCCAGGCCAATAGGCC-----	9405
QY	7800	TTTTCCCTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCCTT	7859
Dd	9406	ATTTCCCTGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTCTCTCTCT	9466
QY	7860	TTTTTCTCTTTTTTTTTCTTTCTTCTTCCTAGTGGTCCACTCTTAGCCCTAGTCAGG	7919
Dd	9466	TCTTTTCTCTTTCTTTCTTTCTTCTTCCTTTAATGAGTGGCTCCACTTAGCCCTAGTCAGG	9528
QY	7920	CTACCTGTGAAGGTCCGTAGCCGCTTGACTGTGACAGAGTGTCTGATACTGCGCTCTG	7979
Dd	9526	CTACCTGTGAAGGTCCGTAGCCGCTAGCTGACAGAGTGTCTGATACTGCGCTCTCTG	9585
QY	7980	CAGATCAAGT 7989	
Dd	9586	CAGATCAATGT 9595	

RESULT 2
 US-08-324-977-31
 Sequence 31, Application US/08324977
 Patent No. 5747739
 GENERAL INFORMATION:
 APPLICANT: OKAYAMA, Hioto
 APPLICANT: FUKE, Isao
 APPLICANT: MORI, Chisato
 APPLICANT: TAKAMIZAWA, Akahisa
 APPLICANT: YOSHIDA, Iwao
 TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
 NUMBER OF SEQUENCES: 50
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 ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &
 ADDRESS: Naughton
 STREET: 1725 K St. N.W. Suite 1000
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
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 PRIOR APPLICATION DATA:
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 FILING DATE: 25-JUN-1990
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 FILING DATE: 31-AUG-1990
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 APPLICATION NUMBER: JP 2-305605
 FILING DATE: 09-NOV-1990
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 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/635,451
 FILING DATE: 28-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Stevens-Smith, Theresa M.
 REGISTRATION NUMBER: 36,281
 REFERENCE/DOCKET NUMBER: 900703D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 659-2930
 TELEFAX: (202) 887-0357
 TELEX: 440142
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8      APPLICANT: MORI, CHISATO
9      APPLICANT: TAKAMIZAWA, AKAHISA
10     APPLICANT: YOSHIDA, IWAO
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15     ADDRESSEE: Armstrong, Westernman, Hattori, McIeland &
16     STREET: 1725 K St. N.W. Suite 1000
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43     FILING DATE: 09-7/635,451
44     ATTORNEY/AGENT INFORMATION:
45     NAME: Stevens-Smith, Theresa M.
46     REGISTRATION NUMBER: 36,281
47     REFERENCE/DOCKET NUMBER: 900703B
48     TELECOMMUNICATION INFORMATION:
49     TELEPHONE: (202) 659-2930
50     TELEFAX: (202) 887-0357
51     TELEX: 440142
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QY	2700	TATCTGTGGGATTCGGACATGCTGTGACCAAGGGGAGAGGGGTGGAGCGCGCATCGTGT	2759
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QY	2760	GCTGGCCACCGCTTACGGCTCCGGATGTGATCCAGTGCACATCCAAATCTGAGAGGT	2819
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Db	2928	GGCTGTCTATATCTGTAGAGATCCCTTCTATGGCAAAAGCATCCCATGAGAGCAT	2987
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D	3048	AAAGCTGTACAGCCTCGGAATCAACGCTGTGGGGATTAACCGGGGCTGATGTGCGT	3107
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D	3108	CATACCAACTATGGAGACGCTGTTCTGTGCACAAAGACGCTCTGATAGAGGGCTATAC	3167
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D	3168	GGGGGACTTTGACTCAATGATGCACGTATACACATGTGTACCCAGACAGTGCATTCAG	3227
Q	3120	CTTGACCCGACCTTGACCATTCATTGAGACGACGACCGGTGCCAAGACGGGTGTACGCTC	3179
D	3228	CTTGATATCCACCTTCACCTTGTAGACGACGACCGGTGCCACAGACGAGTGTGCGCGCTC	3287
Q	3180	GCACGGCGAGGACGAGGACTGTGAGGGGCAAGATGGGCAATTACAGTTTGTGACTTCGAG	3239
D	3288	GCACGGCGGGGATAGACTGTGCAGGGGTAGAGAGGCACTCTACAGTTTGTGACTTCGAG	3347
Q	3240	AGAAAGCCCTCGGGGCAATGTTTCGATTCCTGTGCTGTGTGAGAGTGTCTATGACGCGGCTG	3299
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D	3408	TGCTTGTAGAGGTCACCGCGGCGAGACTGTGATGTTGCGGGCTTACTTGAACAC	3467
Q	3360	ACCAAGGTTGGCCCTGTGCCAGGACCATCTGAGTCTGGAGAGGCTTACTTACAGGCT	3419
D	3468	ACCAAGGTTGGCCCTTGTGCCAGGACCATCTGAGTCTGGAGAGGCTTACTTACAGGCT	3527
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D	3528	CACCCATATAGATCACAACCTTCTTGTCCAGACCAAGCAGGAGAGACACTTCCCTA	3587
Q	3480	CCTGTATGACATACCAAGCTACGGGTGTGGGCGCAGAGGTCACGCTCCATCGTGGGA	3539
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D	3708	GTACAGGCTGGGAGCCGTTCAAGATGAGGTCACCTCTACCCACCCCATATCAAAATACAT	3767
Q	3660	CATGCATCATGTTCGCGCTGACCTGAGAGGTCGTACAGAGACACTGGTGTCTGTAGGGG	3719
D	3768	CATGCATCATGTTCGCGCTGACCTGAGAGGTCGTACATAGACCTGGTGTCTGTAGGGG	3827
Q	3720	AGTCTTACAGCTTGGCCCGGCTATTTCCTGTACAAACAGGACGCTGTATTGTGGCAG	3779
D	3828	AGTCTTACAGCTTGGCCCGGCTATTTCCTGTACAAACAGGACGCTGTATTGTGGGAG	3887
Q	3780	GATCATCTTGTCCGGAAGGCGGCACTATTCGCCAGAGGAAGTCTTTTACCGGAGAT	3839
D	3888	GATTCATCTTGTCCGGAAGGCGGCACTATTCGCCAGAGGAGCTTCTTACCAAGAGTT	3947
Q	3840	CGATAGATGGAAGAGTGGCGCTCACACTCCCTTACATGTGAACAGGAATGACACTGCG	3899
D	3948	CGATGAATATGGAAGAGTGGCGCTGCGACCTCCTTACATGTGAACAGGAATGACACTGCG	4007
Q	3900	CGAACAATTCAAACAGGAAGCAATCGGGTGTCTGCAAAACGCCACCAACCAAGCGAGGCG	3955
D	4008	CGAGCAATTCAAAGCAAGAGGCGCTGGGTTACTGCAAAACGCCACCAACCAAGCGAGGCG	4065
Q	3960	TGCTGCTCCCTGTGGAATTCAGTAGTGGCGAGCCTCTGAAGCCTTCTGGGCGAAGCAT	4015

Db	4068	TGCGCTCCCGTGGTGGAGTCCAAAGTGGGAGGCCCTTGAGACATTTCTGGGGAAAGACAT	4127
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Db	4128	GTGAAATTTATCAGCGGGATACAGTACTTAGAGGCTTATCCACTGTCCCTGGGAAACC	4187
Qy	4080	CGGATAGCACTAGTATGGCAATTCACAGCTCTATACACACCGCGCTACACCCAAACA	4139
Db	4188	CGCATAGCACTAGTATGGCAATTCACAGCTCTATACACACCGCGCTACACCCAAAG	4247
Qy	4140	TACCCCTCTGTTTAACTCCTGGGGGATGGGTGGCCGCCCAACTTGTCTCTCCAGCGC	4199
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Qy	4200	TGCTTTGCTTTCGTAGGCGCCGGCATCGCTGAGCGGCTGTGGGACGATAGGCTTGG	4259
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Qy	4440	CGTGGGCCAGGGAGGGGCTGTGCAGTGATGAACCGGCTGATAGCGTTCGCTTGGCG	4499
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Db	4608	GGGTATATATTTTCCCCCAGCACTATGTGCTTGAGACGAGCGCGCGCGCTGTATC	4667
Qy	4560	TCAGTCTCTCTAGTCTTACCACTACATCAGCTGTGAAGAGGCTTCACACAGTGCATA	4619
Db	4668	TCAGTCTCTCTCAGGCTTACCACTACATCAGCTGTGAAGAGGCTTCACACAGTGCATA	4727
Qy	4620	CGAGACTGCTCCAGCCATGCTCCGCTGTGTGGCTTAAGNATGTTGGGATTGCATATG	4677
Db	4728	TGAAGACTGCTCCAGCCGTTCTCCGCTGTGTGGCTTAAGGAGTGTGGGACTGGATAG	4787
Qy	4680	CAGGCTGTGACTATTTCAAGACCTGGCTCCAGTCCCAAGCTCTCCGCGATTCCGGG	4733
Db	4788	CAGGCTGTGACTACTTCAAGACCTGGCTCCAGTCCCAAGCTCTCCGCGACTACTCTGG	4844
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Db	4848	AGTCCCTTTTCTCGTGCACACCGGGTCAAGGAGTCTGGCGGGGAGCGGCACTAT	4907
Qy	4800	GCAACCACTGGCCATGTGGAGCAGACGATCACGGGCACTGTGAAGAAAGGTTCCATGAG	4855
Db	4908	GCAACCACTGGCCATGTGGAGCAGACGATCACGGGCACTGTCAAGAAAGGTTCCATGAG	4967
Qy	4860	GATCTGGGGCTAGAGACTGTAGTAAACAGCTGGCATGAGAACTTCCCATTAAGCGCTA	4915
Db	4968	GATCTGGGGCTTAAGACTGTAGCAACACAGCTGGCATGAGAACTTCCCATTAAGCGCTA	5027
Qy	4920	CACCAAGGGCCCTGACAGGCTTCCCGGGGCCAAATATTTCAAGGGCGCTGTGGCGGT	4977
Db	5028	CACCAAGGGCCCTGACACCCCTTCCAGGGCCAAACTATTTCAAGGGCGCTGTGGCGGT	5087
Qy	4980	GACTCTAGAGAGTACGTGAGGTATTACGCGGTTGGGGGATTTCATACATAGCAGGCAAT	5033
Db	5088	GGCCCTTAGGAGTACGTGAGGTACAGCGGGTGGGGGATTTCACACTACGTAGCGGCAAT	5144
Qy	5040	GACCACTGACAACGTAAAGTCCCGTGTCAAGTTCCGGCCCCCGAATTTCTTCACAGAAAT	5095
Db	5148	GACCACTGACAACGTAAAGTCCCATCCAGGTTCCGGCTCCGAATTTCTTCGGAGGAT	5207

QY	5100	GGATGGGGTCCGGTTGCGACAGGTACCGCTCCAGCTGTGCAAACCCCTCTACGGGAGAGGT	51159
Db	5208	GGAGGGAGTCCGGTTGCACAGGTACCGCTCCGGCGTGCAGGCGCTCTCTACGGGAGAGGT	5267
QY	5160	CACATTCCTGGTGGGGCTCAATCAATACCTGGTTGGGTACACAGTCCCATCCGAGCCGA	5219
Db	5268	TACATTCAGAGTGGGGCTCAACCAATACCTGGTTGGGTACAGTACATCATCGAGCCGA	5327
QY	5220	ACCGAGCTAGAGAGTGTACTTCATTCGTACACGACCCCTCCCATTTAGCGGAGAGC	5279
Db	5328	ACCGAGTGTAGAGTGTCTCATCTTCATGTCTACACGACCCCTCCCATCATCAGCAGAAAC	5367
QY	5280	GGCTAACGTAAGCTGAGCCGAGGGAGATCCCCCTCTTTGGCCAGACTATCAGCTAGCA	5339
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QY	5340	GCTCTCTGGCCCTTCTTGAAGGCATATGACTTACCGTATACTCTCCCGGAGCTGA	5399
Db	5448	GTTCTTCGCCCTTCTTGAAGGCACATGCACTACCCATGTCTTCGGAGCGCTGA	5507
QY	5400	CCTATGAGAGCCACACTCCTGTGGGCGCAGAGATGGGCGGGAATCACCCCGTGA	5459
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QY	5460	GTCAGAAATAAGTATATTTTGGACTCTTTCGAGCCCTCCACAGCGGAGAGATGA	5519
Db	5568	GTCGGAACAAAGTGTATCTCTGCACTCTTCGACCCGCTTCAGGCGGAGAGATGA	5627
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QY	5580	GCCCATATGGGACAGCCCGGATTACAACCTCCACTGTTAGAGTCTTGAAGAGACCGGA	5639
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Db	5868	GGAGCTGGCTATAGACCTTGGGAGCTCCGATGTGGCGCGTCGACGAGGGGAGCGC	5927
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QY	5880	CTCTCCATGCCCCCTTGAAGGGGAGAGCCGSGGATCCCGATCTCAGAGAGGCTTGG	5939
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QY	5940	GTTACCGTAAAGAGAGGAGCTAGTAGGAGCTGTCTCTCTCTGATGTCTTACACATG	5999
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QY	6000	GACAGGGCCCTGATCACGCCATGCGCTGGGAGGAAACCAAGCTGCGCATATGCACT	6059
Db	6108	GACAGGGCCCTGATCACGCCATGCGCTGGGAGGAAACCAAGCTGCGCATTAAGCGCTT	6167
QY	6060	GAGCAACTCTTGTCTCGTACACCAACTGTGTCTATGTAACATCTCGAGCGCAAG	6119
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QY	6120	CCTGGGACAGAGAGGTCACTTTGACAGACTGCAAGTCTTGAGACGACACTACCGGA	6179
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QY	6340	GGAGCTCCGGAACTATCCAGCAAGCGCGTTAACCACTCCGCTCCGCTGGAGGACTT	6359
Db	6408	GGAGCTCCGGAACTATCCAGCAAGCGCGTTAACCACTCCGCTCCGCTGGAGGACTT	6457
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QY	6540	GATGGAGCTCTATACAGGATTTCCAACTCTCTGGACAGCGGGTGAAGTTCCTGTGA	6589
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Db	7008	GAAAGCTCCAGACACTGCAGATGCTCGTGAAGCGAGACGACTCGTGTATCTGTGAAG	7067
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QY	7200	TTCTCTGGCTAAGCAACATCATGTATGGGCCACTTGTGGCAAGGATATATCTGAT	7259
Db	7308	CTCTCTGGCTAAGCAACATTAATGTATGTGGCCACTTGTGTGGCAAGGATATATCTGAT	7367
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
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APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: McEland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 9007036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 31:
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Db 1968 TACCTTACAGCGCGGACAGAACAGAGTGCAGGGAGAGGTTCAGGTGTTCACACCGC 2027
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Db 2028 AACACATCTTTTCTGGGCACTGGGTCAAGCGCTGTGTGACATCATCATATGTTGC 2087
QY 1980 CGGCTCAAGACCTTGGCGGCGCCAAAGAGGCCAATCACCCAAATGTACACCAATGTGA 2039
Db 2088 TGGCTCAAGACCTTGGCGGCGCCAAAGAGGCCAATCACCCAGATGTACACCAATGTGA 2147
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QY	2280	CACCCGAGGGGATTCGCAAGAGCGGTGGACCTTTGTACCCGTGAGTCTATGAAACCACTAT	2339
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QY	2340	GGGCTCCCGGGTCTACAGGAAACACTGCTCCCTCCGGCCGCTAACCGGAGAAATTCAGGT	2399
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QY	3240	AGAAAGGGCTTGGGCAATGTTCAATTCCTGGGTTCTGTGGAGTGTGTATAGCGGAGGCTG	3299
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 Patent No. 621872
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 APPLICANT: FUKE, ISAO
 APPLICANT: MORI, CHISATO
 APPLICANT: TAKAMIZAWA, AKIHISA
 APPLICANT: YOSHIDA, ISAO
 TITLE OF INVENTION: NON-B, HEPATITIS VIRUS GENOMIC
 TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Armstrong, Westerman, Hattori, McIreland &
 ADDRESS: Naughton
 STREET: 1725 K ST., N.W. Suite 1000
 City: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
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 SOFTWARE: ASCII
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 FILING DATE:
 PRIOR APPLICATION DATA:
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 APPLICATION NUMBER: US/08/324,977
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 APPLICATION NUMBER: JP 2-305605
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 APPLICATION NUMBER: US 08/099,706
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 FILING DATE: 28-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: McIreland, Le-Nhung
 REGISTRATION NUMBER: 31,541
 REFERENCE/DOCKET NUMBER: 900703G
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 659-2930
 TELEFAX: (202) 887-0357
 INFORMATION FOR SEQ ID NO: 31:
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TYPE: nucleic acid
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us-09-315-850-31

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DB 3648 TCAATGTGGAAGTGTCTCATACGGGCTAAGGCTTACGCTGACAGGGGCAAGCGGCTGCT 3707
QY 3600 GTATAGGCTGAGAGCGGTTCAAAAGAGGTTACTACACACACCCCTAATACATATCAT 3659
DB 3708 GTACAGGCTGAGAGCGGTTCAAAAGAGGTTACTACACACACCCCTAATACATATCAT 3767
QY 3660 CATGCAATGATGTGCTGAGCTGAGAGTGTGTACAGAGCAACCGGTTGTGGAGAGCGG 3719
DB 3768 CATGCAATGATGTGCTGAGAGTGTGTGTACAGAGCAACCGGTTGTGGAGAGCGG 3827

QY 3720 AGTCCTAGCAGCTCTGGCCGCGCTATTCCTGTACAAACAGGAGCGTGGTCATTGTGGGACG 3779
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Db 3828 AGTCCTAGCAGCTCTGGCCGCGCTATTCCTGTACAAACAGGAGCGTGGTCATTGTGGGACG 3887
QY 3780 GATCATCTGTCCGGAAGGCGCGCATCATTCGACAGGGAATCCCTTAACCGGAGGT 3839
|||||
Db 3888 GATTATCTGTCCGGAAGGCGCGCATTCGACAGGGAATCCCTTAACCGGAGGT 3947
QY 3840 CGATGAGATGGAAGATGGCCCTCACACCTCCCTTACATCGAACAGGGAATGACGCTGC 3899
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Db 3948 CGATGAAATGGAAGATGGCCCTCACACCTCCCTTACATCGAACAGGGAATGACGCTGC 4007
QY 3900 CGAACATTCACAAAGAAAGCAATGGGTTGCTGCAACACGACCAAGCAGGAGGC 3959
|||||
Db 4008 CGAGCAATTCACAAAGAAAGCGCTGGGTACTGTCAAAACACGACCAAGCAGGAGGC 4067
QY 3960 TGGTGTCCCGTGGTGAATCCAAAGTGGCGACCCCTCGAAGCCTTCTGGCGGAAGCATAT 4019
|||||
Db 4068 TGGTGTCCCGTGGTGAATCCAAAGTGGCGACCCCTCGAAGCCTTCTGGCGGAAGCATAT 4127
QY 4020 GTGGAAATTCATCAGCGGATACATATTTAGCAGGCTTGTCCACTGTGCTGGCAACC 4079
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Db 4128 GTGGAAATTCATCAGCGGATACATATTTAGCAGGCTTGTCCACTGTGCTGGCAACC 4187
QY 4080 CCGGATAGCATCTAGTATGCAATTCACAGCCTATACACAGCCGCTCACACCCACA 4139
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Db 4188 CCGAATAGCATCTAGTATGCAATTCACAGCCTATACACAGCCGCTCACACCCACA 4247
QY 4140 TACCTCTCTGTTTAAATCTTGGGGGATGGTGGCCGCCCACTGCTCTCCAGGC 4189
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Db 4248 TACCTCTCTGTTTAAATCTTGGGGGATGGTGGCCGCCCACTGCTCTCCAGGC 4307
QY 4200 TGGTGTCCCGTGGTGAAGGCGGATCGCTGAGCGGCTGTGGACATAGGCGCTGG 4259
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Db 4308 CCGTGTGGCTTTCGTGGGGCGCGCATCGCCGCTGGCATATGAGCCTTTGG 4367
QY 4260 GAAGTGTCTTGGATATTTTGGCAGTTATGAGCAGGGGTGGCAGGCGGCTGTGGC 4319
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Db 4368 GAAGTGTCTTGGATATTTTGGCAGTTATGAGCAGGGGTGGCAGGCGGCTGTGGC 4427
QY 4320 CTTTAGGTCTAGAGGCGGAGATGCCCTCCACGAGGACGTGGTACTACTCCCTGC 4379
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Db 4428 CTTTAGGTCTAGAGGCGGAGATGCCCTCCACGAGGACGTGGTACTACTCCCTGC 4487
QY 4380 TATCTCTCCCTGGCCCTAGTGTGTGGGGTGTGTGGCAGGATATGCTCGGCA 4439
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Db 4488 CATCTCTCTCCCTGGCCCTAGTGTGTGGGGTGTGTGGCAGGATATGCTCGGCA 4547
QY 4440 CGTGGGCCAGGAGGAGGGGCTGTGAGTGAACCGGCTGATAGGCTGTGGCG 4499
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Db 4548 CGTGGGTCCGGAGAGGGGCTGTGAGTGAACCGGCTGATAGGCTGTGGCG 4607
QY 4500 GGGTAAACAAGTCTCCCCACGCACTATGTGCTAGAGAGCAGCGCTGACAGCGTGCAC 4559
|||||
Db 4608 GGGTAAACAAGTCTCCCCACGCACTATGTGCTAGAGAGCAGCGCGCTGTGCAC 4667
QY 4560 TCGATCTCTCTAGTCTACCATGATGATGCTGTAAGAGGCTTCCACAGTGGATCAA 4619
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Db 4668 TCGATCTCTCTAGTCTACCATGATGATGCTGTAAGAGGCTTCCACAGTGGATCAA 4727
QY 4620 CGAGGATGCTCCACGCACTGTCCGCGCTGTGGCTAAGAGATTTTGGATTGGATATG 4679
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Db 4728 TGAAGATGCTCCACGCACTGTTCGGCGCTGTGGCTAAGAGATTTTGGACTGGATATG 4787
QY 4680 CAGGAGTGTGACTATTTAAGACCTGGCTCAGTCCAAAGCTCTGCGCGAGCTACCTGG 4739
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Db 4788 CAGGAGTGTGACTATTTAAGACCTGGCTCAGTCCAAAGCTCTGCGCGAGCTACCTGG 4847
QY 4740 AGTCCCTTCTCTCATGTCAACGTGGGTAAAGGAGTCTGGCGGCGAGCGCATAT 4799
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Db 4848 AGTCCCTTCTCTCATGTCAACGTGGGTAAAGGAGTCTGGCGGCGAGCGCATAT 4907

QY 4800 GCAAACACCTGCCATGTGAGCACAGATACCGGACATGTGAAAAAGGTTCCATGAG 4859
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Db 4908 GCAAACACCTGCCATGTGAGCACAGATACCGGACATGTGAAAAAGGTTCCATGAG 4967
QY 4860 GATCGGGGGCTAGGACCTGTAGTAACACGTGGCATGGAACATTCCTCCATTACGGCTA 4919
|||||
Db 4968 GATCGGGGGCTAGGACCTGTAGTAACACGTGGCATGGAACATTCCTCCATTACGGCTA 5027
QY 4920 CACCAAGGGGCCCTGACGCGCTCCCGGGCCCAATTAATTCTAGGCGCTGTGGCGGT 4979
|||||
Db 5028 CACCAAGGGGCCCTGACGCGCTCCCGGGCCCAATTAATTCTAGGCGCTGTGGCGGT 5087
QY 4980 GGCTGTGAGAGTACGTGAGGTTAGCGGGGTGGGGATTTCCACTACGTGACGGCAT 5039
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Db 5088 GGCTGTGAGAGTACGTGAGGTTAGCGGGGTGGGGATTTCCACTACGTGACGGCAT 5147
QY 5040 GACCACTGACAAAGTAAAGTGGCGGTGTACAGTTCCGGCCCGCAATTCCTTACAGAGT 5099
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Db 5148 GACCACTGACAAAGTAAAGTGGCGGTGTACAGTTCCGGCTCTGAATTCCTTCTGAGAGT 5207
QY 5100 GATGGGGTGGCGTTCACAGTACGCTCCAGCGGTGCAAAACCCCTCTACGGGAGAGT 5159
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Db 5208 GATGGGGTGGCGTTCACAGTACGCTCCAGCGGTGCAAAACCCCTCTACGGGAGAGT 5267
QY 5160 CACATTCCTGTGCGGGCTCAATCAATTAACCTGTTGGTTCACAGCTCCCATGCGAGCCGA 5219
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Db 5268 TCAATTCAGGTGGGCTCAACCAATTAACCTGTTGGTTCACAGCTCCCATGCGAGCCGA 5327
QY 5220 ACCGAGGTAGAGTGTCTACTTCCATGCTACCGACCCCTCCCAATTAAGGGGAGAC 5279
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Db 5328 ACCGAGGTAGAGTGTCTACTTCCATGCTACCGACCCCTCCCAATTAAGGGGAGAC 5387
QY 5280 GGCTAAGCTAGGCTGAGGAGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCA 5339
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Db 5388 GGCTAAGCTAGGCTGAGGAGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCA 5447
QY 5340 GCTGTCTGGCTTCTCTGTAAGGACATGCACTACCCGTATATCTACCTCCCGAGCTGA 5399
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Db 5448 GTTGTCTGGCTTCTCTGTAAGGACATGCACTACCCGTATATCTCTCCGAGCGCTGA 5507
QY 5400 CCTCATGAGGCGCAACCTCTGTGCGGAGAGATGGGCGGGAATCAACCCCGTGA 5459
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Db 5508 CCTCATGAGGCGCAACCTCTGTGCGGAGAGATGGGCGGGAATCAACCCCGTGA 5567
QY 5460 GTTCAGAAATTAAGTATATTTTGGACTCTTGTGAGCGCTCCCAAGCGGAGGATGA 5519
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Db 5568 GTTCAGAAATTAAGTATATTTTGGACTCTTGTGAGCGCTCCCAAGCGGAGGATGA 5627
QY 5520 GAGGAGATATCGTCTCGCGGAGATCTCGGAGGTCCAGAAATTCCTCTCAGAGAT 5579
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Db 5628 GAGGAGATATCGTCTCGCGGAGATCTCGGAGGTCCAGAAATTCCTCCCGAGGAT 5687
QY 5580 GCCCATATGGCAGCGCGGATTTACACCTCTCAGCTTTAAAGTCTTGAAGACCCGGA 5639
|||||
Db 5688 GCCCATATGGCAGCGCGGATTTACACCTCTCAGCTTTAAAGTCTTGAAGACCCGGA 5747
QY 5640 CTACGCTCTCTAGTGTACAGGGGTGTCAATGTGGCGCTCCCAAGGCGCTCTCGATAC 5699
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Db 5748 CTACGCTCTCTAGTGTACAGGGGTGTCAATGTGGCGCTCCCAAGGCGCTCTCGATAC 5807
QY 5700 ACCCTCAGGGAAGAGAGCGGTTCTCTGTAGAAATCTAACGCTGTCTTCTGCTTGGC 5759
|||||
Db 5808 ACCCTCAGGGAAGAGAGCGGTTCTCTGTAGAAATCTAACGCTGTCTTCTGCTTGGC 5867
QY 5760 GGAAGTCCGCAAAAGACCTTGGAGGCTCGGAATCTGTGGCGCTCGACAGCGACGCGC 5819
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Db 5868 GGAAGTCCGCAAAAGACCTTGGAGGCTCGGAATCTGTGGCGCTCGACAGCGACGCGC 5927
QY 5820 AAGGCGCTCTCTGACACAGCCCTCGAGAGCGCGAGGATCCGAGCTTGTGAGTGTA 5879
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Db 5928 AAGGCGCTCTCTGACACAGCCCTCGAGAGCGCGAGGATCCGAGCTTGTGAGTGTA 5987
QY 5880 CTCTCTCATGTCCCGCTTGAAGGGGAGCGGGGATTCGATCTCAGCGAGCGGCTTG 5939

Db 4727 CTTGATGCCACCTTACCATTTGAGACGACCGTCCCAAGACGAGTGTGCGGCTC 4786
Qy 3180 GCAGCGGAGGACGAGTGTAGGGGACGAGATGGGATTTACAGTTTGTGACTCCAG 3239
Db 4787 GCAGCGGAGGAGTGTAGGACTGGACGGGTAGGACAGGCACTTACAGTTTGTGACTCCAG 4846
Qy 3240 AGAAGCGGCTCGGGCATGTTGCATTCCTGCGTCTGTGCGAGTGTATGACGGGGCTG 3299
Db 4847 AGAAGCGGCTCGGGCATGTTGCATTCCTGCGTCTGTGCGAGTGTATGACGGGGCTG 4906
Qy 3300 TGGTTGTAGAGCTCACGCGCGCGGACGAGCTAGTAGTTGGGGCTTACCTAAACG 3359
Db 4907 TGGTTGTAGAGCTCACGCGCGCGGACGAGCTAGTTAGTTTGGGGCTTACCTAAACG 4966
Qy 3360 ACCAGGCTTGGCCCTGTGCGACGACATCTGAGTTCTGGAGAGCGCTTTACAGGCT 3419
Db 4967 ACCAGGCTTGGCCCTGTGCGACGACATCTGAGTTCTGGAGAGCGCTTTACAGGCT 5026
Qy 3420 CACCCACATAGACGCCCATTTCTGTGCCAGACTAAAGGACGAGGACACTTCCCTA 3479
Db 5027 CACCCATATAGATCACACTTCTGTGCCAGACCAAGGACGAGGACACTTCCCTA 5086
Qy 3480 CCTGTAGCATACAGGCTACGAGTGTGCGGAGGGCTCAGGCTCCACCTCCATCGTGG 3539
Db 5087 CCTGTAGCATACCAAGGACAGGTGTGCGGAGGGCTCAGGCTCCACCTCCATCGTGG 5146
Qy 3540 CCAATGTGGAAGTGTCTCATAGGCTTAAAGCTTACGCTGACAGGGGCAAGCGCTGCT 3599
Db 5147 TCAATGTGGAAGTGTCTCATAGGCTTAAAGCTTACGCTGACAGGGGCAAGCGCTGCT 5206
Qy 3600 GTATAGGCTGGGAGCGCTTCAAAACGAGTTACTACACACACCCATAACCAATACAT 3659
Db 5207 GTACAGGCTGGGAGCGCTTCAAAACGAGTTACTACACACACCCATAACCAATACAT 5266
Qy 3660 CATGAGCATGATGTGGGTGACCTGAGAGTGTGACAGGACCTGGTGTGAGCGG 3719
Db 5267 CATGAGCATGATGTGGGTGACCTGAGAGTGTGACAGGACCTGGTGTGAGCGG 5326
Qy 3720 AGTCTTACAGCTCTGGGCGCGGTATGTGCGTACACAGGAGCGGTGCTATTTGGAGCG 3779
Db 5327 AGTCTTACAGCTCTGGGCGCGGTATGTGCGTACACAGGAGCGGTGCTATTTGGAGCG 5386
Qy 3780 GATCATCTTGTCCGGAAGCGCGCATTCCTCCGACAGGGAAGTCTTTACGGGAGTT 3839
Db 5387 GATCATCTTGTCCGGAAGCGCGCATTCCTCCGACAGGGAAGTCTTTACGGGAGTT 5446
Qy 3840 CGATGAGATGGAAGTGTGCGCTCACAGCTCCCTTACATGGAACAGGGAATGAGCTCGC 3899
Db 5447 CGATGAGATGGAAGTGTGCGCTCACAGCTCCCTTACATGGAACAGGGAATGAGCTCGC 5506
Qy 3900 CGAACATTTCAAAACGGAAGGCAATCGGGTGTCTCAAAACGCAACCAAGCAAGCGAGCG 3959
Db 5507 CGAACATTTCAAAACGGAAGGCAATCGGGTGTCTCAAAACGCAACCAAGCAAGCGAGCG 5566
Qy 3960 TGGCTCTCCCGTGGGAGATCCAGTGTGGGACCGCTGGAAGCTTCTGGGGCAAGCAT 4019
Db 5567 TGGCTCTCCCGTGGGAGATCCAGTGTGGGACCGCTTGAAGCATTTCTGGGGCAAGCAT 5626
Qy 4020 GTGGAATTTTCATCAGCGGAGTACATATTTAGCAGGCTGTCTCATCTGCTGGCGACCC 4079
Db 5627 GTGGAATTTTCATCAGCGGAGTACAGTACTTAGCAGGCTTATCCACTGCTGGGAGCC 5686
Qy 4080 CGCGATAGCATGACTGATGGCATTCACAGCTCTATACACGAGCGCGCTACACCCACACA 4139
Db 5687 CGCGATAGCATGATGATGGCATTCACAGCTCTATACACGAGCGCGCTACACCCACACA 5746
Qy 4140 TACGCTCGTGTTAACATCTGCGGGAGTGGGTGGCGCCCACTTCTCTCCACAGCG 4199
Db 5747 TACGCTCGTGTTAACATCTGCGGGAGTGGGTGGCGCCCACTTCTCTCCACAGCG 5806
Qy 4200 TGGTTGTGTTTGTGAGGCGCGGATGCTGAGCGGCTGTGTGGACGATAGGCTTGG 4259

Db 5807 CGCTTCGAGCTTCTGTGGCGCGGACATCGCCGCTGCGGCTGTGGACGATAGGCTTGG 5866
Qy 4260 GAAGTCTCTGTGATATATTTGGAGGTTATGAGACGAGGGGTGGACGAGCGCTCTGTGC 4319
Db 5867 GAAGTCTCTGTGATATATTTGGAGGTTATGAGACGAGGATGGCGCGCTCTGTGC 5926
Qy 4320 CTTTAAGTCTATGAGCGGCGGAGATGCGCTCCACGAGGAGACTGCGTAACCTCTCC 4379
Db 5927 CTTTAAGTCTATGAGCGGCGGAGATGCGCTCCACGAGGAGACTGCGTAACCTCTCC 5986
Qy 4380 TATCTCTCCCTGGCGCCCTAGTGTGCGGGGTGTGTGGCAGGATACCTAGCTGGCA 4439
Db 5987 CATCTCTCTCTGGCGCCCTAGTGTGCGGGGTGTGTGGCAGGATACCTAGCTGGCA 6046
Qy 4440 CGTGGGCCAGGAGGAGGGCTGTGACGTGATGACCGGCTATAGCTTGTGCTTCGG 4499
Db 6047 CGTGGGTCCGGAGAGGGGCTGTGACGTGATGACCGGCTATAGCTTGTGCTTCGG 6106
Qy 4500 GGGTAAACAGCTTCCGCCACGACACTATGTGCTGAGAGCGAGCTGACAGCATGTCTAC 4559
Db 6107 GGGTAAATATTTTCCGCCACGACACTATGTGCTGAGAGCGAGCGCGAGCGGTGTAC 6166
Qy 4560 TCGATCTCTCTGTGCTTACCATCTACTGACGTGTGAAAGGCTTCCACAGTGAACA 4619
Db 6167 TCGATCTCTCTGACGCTTACCATCTACTGACGTGTGAAAGGCTTCCACAGTGAACA 6226
Qy 4620 CGAGGACTGTCCACGCGCATGCTCGGCTGCTGAGAGATGTTGGATTGATATG 4679
Db 6227 TGAAGACTGTCCACACCGGTGTGCGGCTGTGCTGAGGAGTGTGGAGCTGATAG 6286
Qy 4680 CACGCTGTGACTATTTCAAGACCTGCTCCAGCTCCAGCTCTCTGCGGATTCGCGG 4739
Db 6287 CACGCTGTGACTATTTCAAGACCTGCTCCAGCTCCAGCTCTCTGCGGATTCGCGG 6346
Qy 4740 AGTCCCTCTCTCATGTGTACAGTGGGTACAGGGAGTGTGGCGGGGACGAGCTCAT 4799
Db 6347 AGTCCCTCTCTCATGTGTACAGTGGGTACAGGGAGTGTGGCGGGGACGAGCTCAT 6406
Qy 4800 GCAAAACACTGTGCCATGTGAGCACAGATCACCGGACATGTGAAAAAGGTTCCATGAG 4859
Db 6407 GCAAAACACTGTGCCATGTGAGCACAGATCACCGGACATGTGAAAAAGGTTCCATGAG 6466
Qy 4860 GATCGTGGGCTGTAGAGCTGTAGTACAGCTGGCATGGAACATTTCCCATTAACGTA 4919
Db 6467 GATCGTGGGCTGTAGAGCTGTAGTACAGCTGGCATGGAACATTTCCCATTAACGTA 6526
Qy 4920 CACACGGGCGCTGTACAGCGCTCCCGGCGCAAAATATTTAGAGGCGCTGTGGCGGT 4979
Db 6527 CACACGGGCGCTGTACAGCGCTCCCGGCGCAAAATATTTAGAGGCGCTGTGGCGGT 6586
Qy 4980 GGTCTGTAGAGATGATGAGGTATGCGGGGTGGGGGATTTCCACTAGCTGACGGCAT 5039
Db 6587 GGTCTGTAGAGATGATGAGGTATGCGGGGTGGGGGATTTCCACTAGCTGACGGCAT 6646
Qy 5040 GACCACTGACAAAGTATGCGGTGTACAGTGTCCGGCGCGGAATTTCTTCACAGAGT 5099
Db 6647 GACCACTGACAAAGTATGCGGTGTACAGTGTCCGGCGCGGAATTTCTTCACAGAGT 6706
Qy 5100 GGATGGGTGGGTTGACAGAGTACGCTCCAGCTGCAAAACCTCTTACGGAGAGAGT 5159
Db 6707 GGATGGGTGGGTTGACAGAGTACGCTCCAGCTGCAAAACCTCTTACGGAGAGAGT 6766
Qy 5160 CACATCTCTGTGGGCTCAATCAATACCTGTGGGTGACAGTGTCCATGACGAGCGCA 5219
Db 6767 TACATCTCTGTGGGCTCAATCAATACCTGTGGGTGACAGTGTCCATGACGAGCGCA 6826
Qy 5220 ACCGAGCTAGAGTGTCTCACTTCCATGTCTACGAGCCCTCCACATTGCGCGAGAC 5279
Db 6827 ACCGAGCTAGAGTGTCTCACTTCCATGTCTACGAGCCCTCCACATTGCGCGAGAC 6886
Qy 5280 GGTAGGCTAGGCTGCGGAGGAGTCTCCGCTCTGAGGACGATCACTAGCA 5339
Db 6887 GGTAGGCTAGGCTGCGGAGGAGTCTCCGCTCTGAGGAGCTCTACACTAGCA 6946

QY	5340	GCCTTCGGCCCTTCCTTTAAAGCAAAATGCACTACCCGTATACACTCCCGGAGCGGTGA	5399
Db	6947	GTTGTCTGGCCCTTCCTTTAAAGCCGATGACCTACCCACCATGTCTCTCCGAGCTGA	7006
QY	5400	CCTCATAGAGCCCAACCTCCTGTGGCGGAGAGATGGGCGGGAACATCAACCCGCTGA	5459
Db	7007	CCTCATAGAGCCCAACCTCCTGTGGCGGAGAGATGGGCGGGAACATCAACCCGCTGA	7066
QY	5460	GTCAAGAAATAAAGTGTATTTTGGACCTTCGAGCGCTCCAGCGGAGGAGATGA	5519
Db	7067	GTCCGAATAAAGTGTATCTGTGACTCTTTGCACCCGCTTGAGCGGAGAGATGA	7126
QY	5520	GAGGGAAGTATCCGTTCCGGCGAGATCTCCGAGGTCCAGGAATTCCTCGAGCAT	5579
Db	7127	GAGGGAAGTATCCGTTCCGGCGAGATCTCCGGAATTCAGGAATTCCTCCGAGCAT	7186
QY	5580	GCCCATATGGGACGGCCGGATTATCAACCCCTCAGTGTAGAGTCCTGAAGAGACCCGGA	5639
Db	7187	GCCCATATGGGACGGCCGGATTATCAACCCCTCAGTGTAGAGTCCTGAAGAGACCCGGA	7246
QY	5640	CTACGTCCTCAATGGATACbGgGTGTCCATTCGCGCTCGCAAGSCCCTCCGATAC	5699
Db	7247	CTACGTCCTCAATGGATACbGgGTGTCCATTCGCGCTCGCAAGSCCCTCCGATAC	7306
QY	5700	ACCTCCAGGAGGAAGAGAGCGGTCTCTGTGACAGATCTACCGTCTTTCGCTTGGC	5759
Db	7307	ACCTCCAGGAGGAAGAGAGCGGTCTCTTAACAGAGTCTTCGCTTTCGCTTGGC	7366
QY	5760	GGAGCTCGCCACAAGACCTTGGGACGCTCCGATGTGTGGCGCTGCAGACGGCACGC	5819
Db	7367	GGAGCTCGCTACTAAGACCTTCGCGAGCTCCGAATCATGTGGCGCTGCAGACGGCACGC	7426
QY	5820	AAGGACCTTCCTTACCAGCCCTCCGACAGACGGCGGAGATCCGAGTTGAGTGTGA	5879
Db	7427	GACCGCCTTCTGTACAGGACCTCCGACAGCGTGAACAAGATCCGAGTTGAGTGTGA	7486
QY	5880	CTCTCCATGCCCCCTTGAAGGGAGACCGGGAGATCCCATCTCAAGACGGGTCTG	5939
Db	7487	CTCTCCATGCCCCCTTGAAGGGAGAACCGGGAGACCCCGATCTCAAGACGGGTCTG	7546
QY	5940	GTTACCGTAAAGCAGAGAGCGCTAGTGAAGCGTCTCTCTGATGTCTCAACATG	5999
Db	7547	GTTACCGTAAAGCAGAGAGCGCTAGTGAAGTGTCTCTCTCAATGTCTCAACATG	7606
QY	6000	GACAGCGCCTGATCAACGCCATGTGCTGGGAGAGAAACCAAGCTGCCATCATGCACT	6059
Db	7607	GACAGCGCCTGATCAACGCCATGTGCTGGGAGAGAAACCAAGCTGCCATCATGCACT	7666
QY	6060	GAGCAACCTTTCGTCGTACACACAACCTTGGTCTATGCTACAAATCTTCGAGCGCAG	6119
Db	7667	GAGCAACCTTTCGTCGTACACACAACATGTTTATGCACAACTCTCGAGCGCAGG	7726
QY	6120	CCTGGGAGAAAGAGTCACTTTGACAACTGCAAGTGTCTGGAGACAACTACCGGGA	6179
Db	7727	CCTGGGAGAAAGAGTCACTTTGACAACTGTCAAGTGTCTGGAGACCACTACCGGGA	7786
QY	6180	CGTGTCAAGAGATGAAGGGAAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTGA	6239
Db	7787	CGTGTCAAGAGATGAAGGGAAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTGA	7846
QY	6240	GGAAACCTGTAACTGACGCCCCACACTTGGGCCAATCTAAATTTGGCTATGGGGCAA	6299
Db	7847	GGAAACCTGTGAACTGAGGCCCCACACTTGGGCCAATCTAAATTTGGCTATGGGGCAA	7906
QY	6300	GGACGTCGGAACCTATCCAGCAAGGCGTTAACCACATCCGCTCGCTGTGGAAGACT	6359
Db	7907	GGACGTCGGAACCTATCCAGCAAGGCGTTAACCACATCCATCCGCTGTGGAAGACT	7966
QY	6360	GCTGGAAGACACTGAGACACAAATTGACACCACTATCAAGCAAAAATGAGACTTTTG	6419
Db	7967	GCTGGAAGACACTGAGACCAAAATTGACACCACTATCAAGCAAAAATGAGACTTTTG	8026

QY	6420	CCACCAACACGAGAAAGGGGGCCGCAAGACACTGGCCCTTACCTGATTTCCCAATTGGG	6479
Db	8027	TGTCAAACCCAGAAAGAGAGGCCGTAAAGCCBACCCGCCCTTATCGTATTTCCCAATCTGGG	8086
QY	6480	GGTTCGTGTGTGGGAAAAATGGCCCTTTTACGATGTGGTCTCCACCCCTCCAGCCCGT	6539
Db	8087	AGTCCGTGTGTGGGAAAGATGGCCCTCTATGATGTGGTCTCCACCCCTCCAGGTCGT	8146
QY	6540	GATGGGCTTTCTATAGGAGATCCCAATCTCTCTGTGGAGAGGGGTCCAGTTCCTGGGGA	6599
Db	8147	GATGGGCTCTCTATAGGATTCAGTACTCTCTGGGCAAGGAGTCGAGTTCTCTGGTGA	8206
QY	6600	TGCCGGAAGACAGAAATAGCCCTATGGGGCTTCGCATATACACCCCGCTGTTTTCAGT	6659
Db	8207	TACCTGGAATTCAAAGAAAAAACCCTATGGGGCTTTTCATATGACACTCGCTGTTTCGACT	8266
QY	6660	AACGGTACTGAGATATGACATCCGTGTATAGAGATCAATCTACAAATGTGTACTTGGC	6719
Db	8267	AACGATCACCGAAGAACACATCCGTGTATAGAGATCAATTTACAAATGTGTGACTTGGC	8326
QY	6720	CCCCAAGCCAGACAGGCCCATATAGTGTGTCTACAGAGCGGCTTACATATCGGGGCCCTCT	6779
Db	8327	CCCCAAGCCAGACAGGCCCTTAATAATCGCTCACAGAGCGGCTTATATACGGGGGTCTCT	8386
QY	6780	GACTAATTTCTAAAGGGCAGACTGCGGCTATCGCCGGTGCAGCCGAGCGGTGTTACTGAC	6839
Db	8387	GACTAATTTCTAAAGGGCAGACTGCGGCTATCGCCGGTGCAGCCGAGCGCGTGTCTGAC	8446
QY	6840	GACCAAGCGGGGTATACCTCTCAATGTATACCTTGAAGCGGTGGGGCTCTGCAGCTGC	6899
Db	8447	GACTGTGCTGGGTATACCTCTCAATGTATACCTTGAAGCGGTGGGGCTCTGCAGCTGC	8506
QY	6900	GAAGCTCCAGSAGCTGCACGATGCTCTGTATCGGAGACGACCTGTCTGTTATCTGTGAAG	6959
Db	8507	GAAGCTCCAGSAGCTGCACGATGCTCTGTATCGGAGACGACCTGTCTGTTATCTGTGAAG	8566
QY	6960	CGCGGGACCCCAAGAGACAGAGCCGAGCCTACGSGGCTTCAGCGGAGGTATAGATACATA	7019
Db	8567	CGCGGGACCCCAAGAGAGAGCGGAGCCTACGAGCTTCACGGGAGGTATAGATACGTA	8626
QY	7020	CTCTCTCCCCCTGGGAGACCGGCCCAACAGATTCGACTTGGAGTTGATTAACATCATG	7079
Db	8627	CTCTCTCCCCCTGGGAGACCGGCCCAACAGATTCGACTTGGAGTTGATTAACATCATG	8686
QY	7080	CTCTCTCAATGTGTACGTCCGCGACGATGATGTGGCAAAAGGGTGTACTATCTCACCCG	7139
Db	8687	CTCTCTCAATGTGTGTGGTGGCCACGATGTGATAGGCCAAAAGGGTGTACTATCTCACCCG	8746
QY	7140	TGACCCCAACACCCCTCTGGGCGGGGTGCTGGAGACAGTATAGACACTCCAGTCAA	7199
Db	8747	TGATCCCAACACCCCTCTAGCAGCGGGTGGGTGGAGAACGTATAGACACTCCAGTTAA	8806
QY	7200	TTCCTGGCTAGGCAACATCATCATGTATGCGCCCACTTGTGGGCAAGGATATCTCGAT	7259
Db	8807	CTCTCGGCTAGGCAACATTTATATGTATGCGCCCACTTGTGGGCAAGGATATCTCGAT	8866
QY	7260	GACTCATTTCTTCTCCATCCCTCTAGCTAGGAGAACACTTGA AAAAGCCCTGATTTGCA	7319
Db	8867	GACTCATTTCTTCTCCATCCCTCTAGGCGCAGGAGCAACTTGA AAAAGCCCTGACTGCCA	8926
QY	7320	GATCTACGGGGGCTGTACTCCATTTGAGCCACTTGAACCTACTCCAGATCATTTCAAGCACT	7379
Db	8927	GATCTACGGGGGCTGTACTCCATTTGAGCCACTTGAACCTACTCCAGATCATTTGAAGCACT	8986
QY	7380	CCATGGCCTTAGCCATTTTACCTCCATATTTACTCTCCAGGTGAGATCAATAGGGGTGC	7439
Db	8987	CCATGGCCTTAGCCATTTTACTCTCCATAGTACTCTCCAGGTGAGATCAATAGGGTGGC	9046
QY	7440	TTTCATGGCTCAGGAAGTGTGGGATACCGCCTTGCGAGTCTGGAGACATCGGGCCAGAG	7499
Db	9047	TTTCATGGCTCAGGAAGTGTGGGATACCACTTGCGAGTCTGGAGACATCGGGCCAGAG	9106
QY	7500	TGTCGCGCTAGGCTACTGTCCACGGGGGAGAGGCTGCCACTTGTGTGGCAAGTACTCTT	7559

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Db	9167	CGTCCGCGCTAGAGGTACTGTCTCCACAGGAGGAGGAGGCGCCACTTGTGGCAATAACTCTT	9166
07	7550	CAACTGGGACAGTAGGACCCACAGCTCAACTCAGTCCATCCCGGCTGGTCTCCCACTTGA	76119
Db	9167	CAACTGGGACAGTAAACCCAACTTTAACTCATCTCAATCCGCGTGGCTCCGCTGGA	9226
07	7620	TTTATCCAGCTGTGTTCTCTCTCTGTTACAGCGGGGAGACATATATCAAGCCTGTCTCG	7679
Db	9227	CTGTCTCCGCGCTGTGTCTGTCTGTCTGTTACAGCGGGGAGACATATATCAAGCCTGTCTCG	9286
07	7680	TGCCCCAGCCCGCGTGTCTATGTGTGTGCTACTCTCTACTTCTGTAGGGTAGAGCATTA	7739
Db	9287	TGCCCGACCCCGTGTGTCTATGTGTGTGCTACTCTCTACTTCTGTAGGGTAGAGCATTA	9346
07	7740	TCTACTCTCCCAACCGATGAACGGGGAGCTAAACACTCTCAGGCCAATAGCCATCTCTTT	7799
Db	9347	CTGTCTCCCGACCGATGAACGGGGAGATTAACACTCTCAGGCCAATAGCCATCTCTTT	9406
07	7800	TTTTCCCTT 7809	
Db	9407	TTTTTTTTT 9416	
RESULT 7			
: Sequence 1, Application US/08384616			
: Patent No. 5847101			
: GENERAL INFORMATION:			
: APPLICANT: OKAYAMA, HIROTO			
: APPLICANT: FUKU, ISAO			
: APPLICANT: MORI, CHISAO			
: APPLICANT: TAKAMIZAWA, AKAHISA			
: APPLICANT: YOSHIDA, IWAO			
: TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC			
: TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE			
: NUMBER OF SEQUENCES: 50			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &			
: ADDRESS: Naughton			
: STREET: 1725 K St. N.W. Suite 1000			
: CITY: Washington			
: STATE: D.C.			
: COUNTRY: U.S.A.			
: ZIP: 20006			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Diskette, 3.5 in, 1.44MB			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0			
: SOFTWARE: ASCII			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/384,616			
: FILING DATE:			
: CLASSIFICATION: 424			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/769,996			
: FILING DATE: 02-OCT-1991			
: APPLICATION NUMBER: JP 2-167466			
: FILING DATE: 25-JUN-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: JP 2-230921			
: FILING DATE: 31-AUG-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: JP 2-305605			
: FILING DATE: 09-NOV-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 07/635,451			
: FILING DATE: 28-DEC-1990			
: ATTORNEY/AGENT INFORMATION:			
: NAME: Stevens-Smith, Theresa M.			
: REGISTRATION NUMBER: 36,281			
: REFERENCE/DOCKET NUMBER: 900703B			
: TELECOMMUNICATION INFORMATION:			

QY	1800	CATGGGCGCCATTATACGGCTACTCCCAACAGACGGAGGAGGCTTACTAGTGCATCATCAC	1859
DB	3407	CTCTGCGCCCATACGCGCTACTCCCAACAGACGGAGGAGGCTTACTAGTGCATCATCAC	3466
QY	1860	TAGCCTCACAGGCCGGGACAGAACAGTGCAGAGGAGAGGTCCAGTGGTCTCCACCCG	1919
DB	3467	TAGCCTTACAGGCCGGGACAGAACAGTGCAGAGGAGAGGTTCAGTGGTCTCCACCCG	3526
QY	1920	AACCAATCTTTCTTGGCAGCTGGCGTCAATGGCTGTGTGAGACTCTATCATATGATGC	1979
DB	3527	AACCAATCTTCTTGGCAGCTGGCGTCAACGGCTGTGTGAGACGTTTACATGATGTC	3586
QY	1980	CGGCTCAAGACCCCTTGCGGCCCAAGAGGCCCAATACCCAATGTACACCATGTGGA	2039
DB	3587	TGGCTCAAAACCTTAGCGCGCCAAAGGGGCAATCCAGATGTACATATGTGGA	3646
QY	2040	CCAGACCTGTGTGGCGGGAAGGCGCCCGGGCGGCTGTGACACCATGACACTG	2099
DB	3647	CCAGACCTGTGTGGCTGGCGGAAGGCGCCCGGGCGGCTGTGACACCATGACACTG	3706
QY	2100	CGGAGCTGGAGCTTTACTTGTACAGAGCATCCGATGTATTCGGGTGGCGCGCG	2159
DB	3707	TGGAGCTGGAGCTTTACTTGTGTACAGAGCATCTGACGTCAATTCGGGTGGCGCGCG	3766
QY	2160	GGGCGACAGAGGGGAGGAGCTTACTCCCGAGGCGGCTGTCTCACTTGAAGGCTCTTC	2219
DB	3767	GGGCGACAGTAGGGGAGGAGCTGTCTCTCCCGAGGCTGTCTCTCACTTGAAGGCTCTTC	3826
QY	2220	GGGCGGTCTACTGTCTGCCCCCTCGGGGAGAGCTGTGGGCACTTTTGGGGTGGCGGTG	2279
DB	3827	GGGCGGTCTACTGTCTGCCCCCTCGGGGAGAGCTGTGGGCACTTTTGGGGTGGCGGTG	3886
QY	2280	CACCGGAGGGGTGGCGAAGCGGTGACTTTTACCCGCTGCAAGTCTATGGAACCACTAT	2339
DB	3887	CACCGGAGGGGTGGCGAAGCGGTGACTTTTACCCGCTGCAAGTCTATGGAACCACTAT	3946
QY	2340	GGGTCCTCCGCTTTCACGAGCAACTGTCCTCCCTCGGCGGTACCGAGACATTCAGGT	2399
DB	3947	GGGTCCTCCGCTTTCACGAGCAACTGTCCTCCCTCGGCGGTACCGAGACATTCAGGT	4006
QY	2400	GGCCATCTACAGCCGCCCTACTGTAGCGGCAAGAGCACTAAGTGCACGCGTGGGTATGC	2459
DB	4007	GGCCATCTACAGCGCTCCCACTGCAAGCGGCAAGAGTACTAAGTGCACGCGTGGGTATGC	4066
QY	2460	AGCCCAAGGATTAAGTGTCTTCTGTGAACCCGTCGCGCGGACACCTAGGTTTCGG	2519
DB	4067	AGCCCAAGGATTAAGTGTCTTCTGTGAACCCGTCGCGCGGACACCTAGGTTTCGG	4126
QY	2520	GGCGTATATGTCTAAGGACATGTATCAACCTTAACATCAGAACCGGGGTAAAGACAT	2579
DB	4127	GGCGTATATGTCTAAGGACATGTATCAACCTTAACATCAGAACCGGGGTAAAGACAT	4186
QY	2580	CACCAAGGTTGCCCATCACTACATCCATTAAGCAAGTTTCTTGGCGAGGTTGGTTG	2639

Db 4187 TACCACAGGCGCCCGCTACATCTACTACCTATGCGAAGTTTCTGCGCATGSGTTG 4246
QY 2640 CTCGTGGGGGCGCCTATGACATCATATATGATGATGATGCGCCTACCTACTGACCGAC 2699
Db 4247 CTCGTGGGGGCGCCTATGATCATCATATATGATGATGATGCGCCTACCTACTGACCTAC 4306
QY 2700 TATCCGCGGCGATGCGGACAGTCTCTGAGCAACGCGAGAGCGGTGGAGCGGACTGCGCT 2759
Db 4307 AATCTTGGGCGATGCGGACAGTCTCTGAGCAACGCGAGAGCGGTGGAGCGGACTGCGCT 4366
QY 2760 GCTCGCCACCGCTACGCTCCCGGATCGGTACCGGTGCGCAGATCCAAACATCGAGAGGT 2819
Db 4367 GCTCGCCACCGCTACGCTCCCGGATCGGTACCGGTGCGCAGATCCAAACATCGAGAGGT 4426
QY 2820 GGTCTGTCTCAGACCTGAGGAATCCCTTTATGCGAAGCGATCCCATCGAGACAT 2879
Db 4427 GGGCTGTCTTAATCTGAGAGATCCCTTCTATGCGAAGCGATCCCATCGAGACAT 4486
QY 2880 CAAGGGGGGGAGGACCTCATTTTCTGCCATTCCAGAAGAATGTGATGAGCTCGCGC 2939
Db 4487 CAGGGGGGGAGGACCTCATTTTCTGCCATTCCAGAAGAATGTGATGAGCTCGCGC 4546
QY 2940 GAAGCTGTCCGGCTCGGACTCAATGCTTACCATTTACCGGGGCTTGTATGATCCGT 2999
Db 4547 AAAGCTGTCAAGGCTCGGAATCAACGCTGTGGCGTATTACCGGGGGCTGATGTGCTGT 4606
QY 3000 CATACCACTAGGAGAGAGATCATTTGCTAGCAGCGAGCGCTCATATGAGGGCTTAC 3059
Db 4607 CATACCACTAGGAGAGAGATCATTTGCTAGCAGCGAGCGCTCATATGAGGGCTTAC 4666
QY 3060 CGGCGATTTCGACTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3119
Db 4667 GGGCGATTTCGACTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4726
QY 3120 CCGGAGCGGACCTTACCATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3179
Db 4727 CTTTGATCCACCTTCACTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4786
QY 3180 GCAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3239
Db 4787 GCAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4846
QY 3240 AGAAGCGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3299
Db 4847 AGAAGCGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4906
QY 3300 TGGTGTGTAGAGCTACGCGCGCGCGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACAC 3359
Db 4907 TGGTGTGTAGAGCTACGCGCGCGCGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACAC 4966
QY 3360 ACCAGGTTCCCGCTCTGCGAGAGACCTGAGGTTCTTGGAGAGCGTTTACAGGCT 3419
Db 4967 ACCAGGTTCCCGCTCTGCGAGAGACCTGAGGTTCTTGGAGAGCGTTTACAGGCT 5026
QY 3420 CACCAATAGAGCGCCATTCTTGTCCAGACTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3479
Db 5027 CACCAATAGAGCGCCATTCTTGTCCAGACTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5086
QY 3480 CTTGTGTAGCATACGAGCTACGTTGTGCGGAGAGGCTCAGGCTCCACCTCCATCTGTGGA 3539
Db 5087 CTTGTGTAGCATACGAGCTACGTTGTGCGGAGAGGCTCAGGCTCCACCTCCATCTGTGGA 5146
QY 3540 CCAATGTGGAAGTGTCTCATAGGCTAAAGCTTACGCTGACGAGGCGCAACCGCTGCT 3599
Db 5147 TCAATGTGGAAGTGTCTCATAGGCTAAAGCTTACGCTGACGAGGCGCAACCGCTGCT 5206
QY 3600 GTATAGGCTGGAGCGCTTAAAAAGAGGTTACTACCAACAGCCCATTAACCAATACAT 3659
Db 5207 GTATAGGCTGGAGCGCTTAAAAAGAGGTTACTACCAACAGCCCATTAACCAATACAT 5266
QY 3660 CATGGCATGATGCGGCTACCTGAGAGGCTGACAGACACCTGGTCTGTAGGCGG 3719
Db 5267 CATGGCATGATGCGGCTACCTGAGAGGCTGACAGACACCTGGTCTGTAGGCGG 5326

QY 3720 AGTCTTAGAGCTGTGGCGCGCTATTGCTGTGACAAACAGGCGGTGATGTTGGGCGAG 3779
Db 5327 AGTCTTAGAGCTGTGGCGCGCTATTGCTGTGACAAACAGGCGGTGATGTTGGGCGAG 5386
QY 3780 GATCATCTTGTCCGGAAGGCGCGCCATCATTCGCGACAGGGAAGTCTTACCGGAGTT 3839
Db 5387 GATCATCTTGTCCGGAAGGCGCGCCATCATTCGCGACAGGGAAGTCTTACCGGAGTT 5446
QY 3840 CGATGAGATGAGAGTGTGCGCTCAGACCTCCCTTACATTCGAAGAGGAATGACGCTGCG 3899
Db 5447 CGATGAGATGAGAGTGTGCGCTCAGACCTCCCTTACATTCGAAGAGGAATGACGCTGCG 5506
QY 3900 CGACATTTCAACAGAGAGGCAATCGGCTTGTGCGAAGAGCCACCAAGAGCGGAGGC 3959
Db 5507 CGACATTTCAACAGAGAGGCAATCGGCTTGTGCGAAGAGCCACCAAGAGCGGAGGC 5566
QY 3960 TGTGCTCCCGTGTGTGAATCCAAAGTGGCGGAGCCGCAACCTTCTTGGGGAAGCATAT 4019
Db 5567 TGTGCTCCCGTGTGTGAATCCAAAGTGGCGGAGCCGCAACCTTCTTGGGGAAGCATAT 5626
QY 4020 GTGGAATTTATCAGCGGAGATCAATATTATACAGGCTTGTCCACTGTGCTGCAACCC 4079
Db 5627 GTGGAATTTATCAGCGGAGATCAATATTATACAGGCTTGTCCACTGTGCTGCAACCC 5686
QY 4080 CGCGATAGCATCTGATGAGGCAATTCACAGCCTCTATCACAGCCCGCTACCCACACA 4139
Db 5687 CGCATAGCATCTGATGAGGCAATTCACAGCCTCTATCACAGCCCGCTACCCACACAAG 5746
QY 4140 TACCTCTCTGTTAATCATCTGAGGAGGATGGGTGCGCCCAACTGTCTCTCCAGGCG 4199
Db 5747 TACCTCTCTGTTAATCATCTGAGGAGGATGGGTGCGCCCAACTGTCTCTCCAGGCG 5806
QY 4200 TGGT 4259
Db 5807 TGGT 5866
QY 4260 GAAGGCTCTTGT 4319
Db 5867 GAAGGCTCTTGT 5926
QY 4320 CTTTAAGTATAGGCGGAGATGCGCTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4379
Db 5927 CTTTAAGTATAGGCGGAGATGCGCTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5986
QY 4380 TATCTCTCTCTGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4439
Db 5987 TATCTCTCTCTGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6046
QY 4440 CGTGGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4499
Db 6047 CGTGGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6106
QY 4500 GGGTAAACAGTCTCCCGCAGCAGCTATGCTGTGAGAGCGAGCGTGAAGCAGCTGTAC 4559
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QY 4560 TCAGATCTCTAGTCTTACATCACTCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4619
Db 6167 TCAGATCTCTAGTCTTACATCACTCAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6226
QY 4620 CGAGGAGCTCTCAGCGCATGCTCGGCTGTGAGGCTAAGAGATGTTGGAGTGTGATATG 4679
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QY 4680 CAGGCTGTACAGATTTAAGACCTGAGTCCAGTCAAGCTCTGCGCGATTCGCGG 4739
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QY 4740 AGTCCCTTCTTCTCATGTCAACGTTGTACAGGAGTGTGCGGGGCGAGCGCATAT 4799
Db 6347 AGTCCCTTCTTCTCATGTCAACGTTGTACAGGAGTGTGCGGGGCGAGCGCATAT 6406

QY	4800	GCACACCTGGCCATGTGGAGACAATGATCCGCGACATGTGAAAAAGTTCCATGAG	4855
QY	4800	GCACACCTGGCCATGTGGAGACAATGATCCGCGACATGTGAAAAAGTTCCATGAG	4855
Db	6407	GCAACCACTGGCCATGTGGAGACAATGATCCGCGACATGTGAAAAAGTTCCATGAG	6466
QY	4860	GATCGTGGGCGCTGAGACCTGTAGTAACACGCGGATGGAACATTTCOCATTACGGCTA	4919
Db	6467	GATCGTGGGCGCTGAGACCTGTAGTAACACGCGGATGGAACATTTCOCATTACGGCTA	6526
QY	4920	CACCAGGGGCGCTGACACCGCTCCCGGGCGCCAAATTATCTAGGGGCTGTGGCGGT	4979
Db	6527	CACCAGGGGCGCTGACACCGCTCCCGGGCGCCAAATTATCTAGGGGCTGTGGCGGT	6586
QY	4980	GGCTGCTGAGAGATACGTGGAGGTACGGGGGTGGGGGATTTCACATACGTGACGGGCAT	5039
Db	6587	GGCGCGTAGAGATACGTGGAGGTACGGGGGTGGGGGATTTCACATACGTGACGGGCAT	6646
QY	5040	GACCACTGACACGTAAATGCCCCGTGTAGTTCCGGCCCCCGCAATTCTTCACAGAGT	5099
Db	6647	GACCACTGACACGTAAATGCCCCGTGTAGTTCCGGCCCCCGCAATTCTTCACAGAGT	6706
QY	5100	GGATGGGGTCCGGTTGACACGAGTACGCTCCACGCTGCAAAACCCCTCTACGGAGAGGT	5159
Db	6707	GGAGGGAGTCCGGTTGACACGAGTACGCTCCGGCGTGCAGGCTCTCTCTACGGAGAGGT	6766
QY	5160	CACATTCCTGGTGGGCTCAATCATACCTGGTTGGGTACAGCTCCCATGCGAGCCGA	5219
Db	6767	TACATTCAGAGTGGGCTCAACCAATACCTGGTTGGGTACAGCTACCATCGAGCCGA	6826
QY	5220	ACCGGAGTAGAGAGTGTACTCTCCATGCTACACCAACCCCTCCCACTTACGGGGAGAC	5279
Db	6827	ACCGGAGTAGAGAGTGTACTCTCCATGCTACACCAACCCCTCCCACTTACGGGGAGAC	6886
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Db	6887	GGCTAACCGTAGAGTGGCGAGGGAGTCCCGCTCCTTGGCCACCTCATCAGCTAGCCA	6946
QY	5340	GCTGTCTGGCGCTTCTTTGAAGGCAACATGACACTACCGCTCATGACTCCCCGGAGCTGA	5399
Db	6947	GTTGTCTGGCGCTTCTTTGAAGGCAACATGACACTACCGCTCATGACTCCCCGGAGCTGA	7006
QY	5400	CCTATGAGAGCAACTCTGTGGGGAGAGATGSGGCGGAGCAATCACCCGCTGGA	5459
Db	7007	CCTATGAGAGCAACTCTGTGGGGAGAGATGSGGCGGAGCAATCACCCGCTGGA	7066
QY	5460	GTCAGAAATAGGTAGTAATTTTGAAGCTTTTCGAGCGCTCCACAGCGGAGAGATGA	5519
Db	7067	GTCAGAAATAGGTAGTATCTCTCGAGACTTTTCGAGCGCTCCACAGCGGAGAGATGA	7126
QY	5520	GAGGAGATATCCGTTCCGGCGGAGATATCGGCGGAGGTCCAGAAATTCCTCGAGCAT	5579
Db	7127	GAGGAGATATCCGTTCCGGCGGAGATATCGGCGGAGGTCCAGAAATTCCTCGAGCAT	7186
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Db	7187	GCCCATATGGGACAGCCCGGATTACAACCTCCACTGTTAGAGTCTCTGAGAGCCCGGA	7246
QY	5640	CTAGCTCCCTCCAGTGGTAAACAGGGGTGTCAATTGCGGCTGCGCAAGCCCCCTCCGATAC	5699
Db	7247	CTAGCTCCCTCCAGTGGTAAACAGGGGTGTCAATTGCGGCTGCGCAATTAAGCCCCCTCCGATAC	7306
QY	5700	ACCTCCACGAGAGAGAGAGAGGTTGCTGTGAGATATACCGTGTCTTGCTGCTTGGC	5759
Db	7307	ACCTCCACGAGAGAGAGAGAGGTTGCTGTGAGATATACCGTGTCTTGCTGCTTGGC	7366
QY	5760	GGAGCTGGCCACAAAGACTTTGGAGACTTCCGATGCTGTGGCGGCTGACAGGGGACAGGC	5819
Db	7367	GGAGCTGGCTACTAAAGACTTTGGCGCACTCCGATATATGGCGCTGACAGGGGACAGGC	7426
QY	5820	AACGGCTCTCTAGACAGCCCTCCGACGACGGCGAGCGGGAGTCCGAGGTGAGTGTGATGCTA	5879
Db	7427	GACGCGCTTCTCTAGACAGCGCTCCGACGACGGGTGACAAAGAGTCCGAGGTGAGTGTGATGCTA	7486
QY	5880	CTCTCTCATGCCCCCTTAAGGGGAGGCCGSGGAGTCCCGATCTTACGACGCGCTTGG	5939

Db	7487	CTCTCCATCCCCCTTGGAGGGGAACCGGGGGACCCCGCATCTCAATGAGGGGCTCTG	7546
QY	5940	GTCTACCGTAAGCGAGAGGCTAGTGAAGACGTGCTTGTGCTCGATGTCTTACACATG	5999
Db	7547	GTCACCGGTAGAGAGAGAGCTAGTGAAGATGTGCTGTGCTCAATGTCTCTACATG	7606
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Db	7607	GACAGGGCCCTTATCAACGGCATGGCTCGGGAGGAACCAAGCTGCCCATCAACGGCTT	7666
QY	6060	GAGCACTCTTGTCTCGTCACCAACACTTGGTCTATGTACACATCTCCAGCGCAG	6119
Db	7667	GAGCACTCTTGTCTCGGCACCATCAATGTGTTATGCGACACATCTCCAGCGAGG	7726
QY	6120	CCCTGGCAGAACAGAGGTCACTTTATACAGACTGCGAGGCTCGAGCGACACTACCGGA	6179
Db	7727	CTCTGGCAGAACAGAGGTCACTTTATACAGACTGCGAGTCTCGAGCGACACTACCGGA	7786
QY	6180	CGTCTCTAAGAGATGAAGCGAGGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGA	6239
Db	7787	CGTGCTCAAGAGATGAAGCGAGGCGTCCACAGTTAAGGCTAAACTCTATCCGTAGA	7846
QY	6240	GGAAGCTGTAGACTGACGCCCCACATTCGGCCAGATTAATTTGGCTATGGGCGAA	6299
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QY	6300	GGAGCTCCGGAACCTATCCAGAGGCGCTTAACCACTCCGCTCCGTGTGAAGAGATT	6359
Db	7907	GGAGCTCCGGAACCTATCCAGAGGCGCTTAACCACTCCGCTCCGTGTGTGAAGAGATT	7966
QY	6360	GCTGGAAGACACTGAGACACCAATTGACACACCATCATGTCGCAAAAATAGAGTTTTCTG	6419
Db	7967	GCTGGAAGACACTGTGACCAATTTGACACACCATCATGTCGCAAAAATGAGGTTTTCTG	8026
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Db	8027	TGTCACACCGAGAGAGGAGGCGGTAGCCAGCGCCCTTATTCGATTTCCGAGACTGGG	8086
QY	6480	GGTTCGTGTGTGCGAGAAAATGGCCCTTTACGATGTGTCTCCACCCTCCCTCAGGCGGT	6539
Db	8087	AGTCCGGTGTATGCGAGAAATGGCCCTCTATGTGTGTCTCCACCCTCCCTCAGGCTGT	8146
QY	6540	GATGGGCTCTTCAAGGATTTCCAAATCTCCTGAGCAGGGGTGAGTTCTGTGTGA	6599
Db	8147	GATGGGCTCTCTAAGGATTTCCAGTCTCCTGAGGAGCGAGTGTGAGTTCTGTGTGA	8206
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QY	6660	AACGCTCACTAGATATACATCCGTGTGAGAGGTAAATCTACCATCTTTGACTTGGC	6719
Db	8267	AACGCTCACTAGATATACATCCGTGTGAGAGGTAAATTTACCATCTTTGACTTGGC	8322
QY	6720	CCCCGACCCGAGACGCCATTAAGGTGTGCTCAAGAGCGGCTTTACATGGGGGCCCTCT	6779
Db	8327	CCCCGACCCGAGACGCCATTAATTCGTCAAGAGCGGCTTTATATGGGGGTCCTCT	8386
QY	6780	GACTAATTTCTAAGGCGCAAGACTGCGGCTATCGCCGGTGC CGCGGAGCGGTGTACTGAC	6833
Db	8387	GACTAATTTCTAAGGCGCAAGACTGCGGCTATTCGCCGGTGC CGCGGAGCGGTGTACTGAC	8448
QY	6840	GACCGGCTGGGTATACCTCATCATGTATTCTTGAAGGCGCGTGGGCTGTGAGCTGAC	6899
Db	8447	GACTGAGCTGGGTATACCTCATCATGTATTCTTGAAGGCGCTGTGAGCTGTGAGCTGAC	8506
QY	6900	GAAAGCTCCAGGACTGCAAGATGTCTGTTATGCGAGAGCAAGCTTGTGTTATCTGTGAAG	6959
Db	8507	GAAAGCTCCAGGACTGCAAGATGTCTGTTATGCGAGAGCAAGCTTGTGTTATCTGTGAAG	8566
QY	6960	CGCGGGAGCCCAAGAGAGAGGAGACCTTAGGGGCTTACGAGAGGCTATACTAGATA	7019

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Page 24

Db 8567 GCGGGGAACCCAGAGAGCGGCGAGCCCTACGAGCTTTACGAGAGCTATGACTAGGTA 8626
QY 7020 CTCTGCCCCCCTTGGGAGACCCGCCAAACAGATACGAGCTTGGAGTTGATTAACATCATG 7079
Db 8627 CTGCGGCCCCCGGGGAGCCCGCCCAACAGATACGAGCTTGGAGCTTGAATCATCATG 8686
QY 7080 CTCTGCAATGTGTGATCGCGGACGATGATCGGCAAAAGGTGTACTATCTCACCCG 7139
Db 8687 TTCTTCCATATGTGTGCTGCGCCACGATGATCGGCAAAAGGTGTACTATCTCACCCG 8746
QY 7140 TGACCCCAACACCCCTTGGCGGGCTGCGGAGACAGCTAGACACACTCCAGTCA 7199
Db 8747 TGATCCCAACACCCCTTGGCGGGCTGCGGAGACAGCTAGACACACTCCAGTCA 8806
QY 7200 TTCTGAGCTAGGCAACATCATGATGAGCCCACTTGTGGGCAAGATGATCTGAT 7259
Db 8807 CTCTGAGCTAGGCAACATCATGATGAGCCCACTTGTGGGCAAGATGATCTGAT 8866
QY 7260 GACTCATTTCTCTCCATCTCTTCTAGCTAGGCAAGCAACTTGAAGCCCTAGATGTA 7319
Db 8867 GACTCATTTCTCTCCATCTCTTCTAGCTAGGCAAGCAACTTGAAGCCCTAGATGTA 8926
QY 7320 GATCTACGGGSCCTGTACTCTCATTGAGCCACTTGACCTACCTAGATCATTCAGACT 7379
Db 8927 GATCTACGGGSCCTGTACTCTCATTGAGCCACTTGACCTACCTAGATCATTCAGACT 8986
QY 7380 CCATGGCCTTACGCAATTTTACCTCATGATGATGATGATGATGATGATGATGATGAT 7439
Db 8987 CCATGGCCTTACGCAATTTTACCTCATGATGATGATGATGATGATGATGATGATGAT 9046
QY 7440 TTCAATGCTCAGAGAACTTGGGGTACCGCCCTTGGAGCTTGAAGATCGGCGCAGAG 7499
Db 9047 TTCAATGCTCAGAGAACTTGGGGTACCGCCCTTGGAGCTTGAAGATCGGCGCAGAG 9106
QY 7500 TGTCCGCTAGGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 7559
Db 9107 TGTCCGCTAGGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 9166
QY 7560 CAAGTGGGAGTAAAGACCAAGCTCAAACTCACTCACTCACTCACTCACTCACTCACT 7619
Db 9167 CAAGTGGGAGTAAAGACCAAGCTCAAACTCACTCACTCACTCACTCACTCACTCACT 9226
QY 7620 TTATATCCAGCTGT 7679
Db 9227 CTGTGCTGCTGT 9286
QY 7680 TGCCGAGCCCGCTGT 7739
Db 9287 TGCCGAGCCCGCTGT 9346
QY 7740 TCTACTCCCAACCGATGAGCGGAGGCTAAACACTCCAGGCAATAGGCAATCTCTGTT 7799
Db 9347 CCTGCTCCCAACCGATGAGCGGAGGATTAACACTCCAGGCAATAGGCAATCTCTGTT 9406
QY 7800 TTTTCCCTT 7809
Db 9407 TTTTCTTTT 9416

RESULT 8
US-08-904-686A-1
Sequence 1, Application US/08904686A
Patent No. 5998130
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FURE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Armstrong, Westernman, Hattori, Mclelland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., 1.44mb
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mclelland, Le Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA from genomic RNA
FEATURE:
NAME/KEY: CDS
LOCATION: 333..9362
US-08-904-686A-1
Query Match 65.3%; Score 5218; DB 2; Length 9416;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5515; Conservative 0; Mismatches 495; Indels 0; Gaps 0;
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Db 3407 CCTGGGCTTATCAGGCTTACTCCCAACAGACGCGGAGGCTTACTGGCTGCTCATCATC 3466
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Db 3467 TAGCTCAGAGCGCGGAGACAGGAGTGTGAGGAGGTGAGGTGTGTCCACCGC 3526
QY 1920 AACACATCTTCTGTGCGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1979
Db 3527 AACACATCTTCTGTGCGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3586
QY 1980 CGGCTCAAGAGCCCTTGGCGGCGCCAAAGGAGGCAATGATGATGATGATGATGATGATG 2039

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Db 3647 CCAGAGACCTGCTGGGGCTGGGCAAGGCCGCCGGGGGGCGGCTTCCTTAGACATGACACTG 3706
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Db 3707 TGGCAGCTCAAGACCTTACTTGGTCAAGAGACATGCTGACGTCATTCGGGTGCGCCGGCG 3766
QY 2160 GGGGAGACAGAGGGGGAGCCTTACTTCCGCCAGGCCGCTTCCTACTTGAAGGGCTTCG 2219
Db 3767 GGGGAGACAGTAGGGGGAGCCTTCTCCGCCAGGCCGCTTGTCTACTTGAAGGGCTTCG 3826
QY 2220 GGGGAGCTCAAGCTGCTGCCCCCTCGGGGCAAGCGCTGTGGGCACTCTTTCGGGGCTGCCGCTG 2279
Db 3827 GGGTGTGTCACAGCTGCTTGGCCCCCTTCGGGGCAAGCGCTGTGGGCACTCTTTCGGGGCTGCCGCTG 3886
QY 2280 CACCCGAGGGGTTGCCAAGGCGGTGGACTTGTACCCGTCGACTATATGGAACCACTAT 2339
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Db 3947 GCGGTCTCCGCTCTTTCACGAGCAACTGCTCCCTCCGGCGGTACCCGACACATTTCCAGST 4006
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QY 3000 CATACCAACTAGCGAGAGCGTATGCTGATGCAAGGAGCGCTTATGAGAGCGGCTTAC 3059
Db 4607 CATACCAACTAGCGAGAGCGTATGCTGATGCAAGGAGCGCTTGTGATGAGAGCGGCTTAC 4666
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Db 4907 TGGTGTAGAGAGCTACAGCCGCCGAGACCTAGTTAGTTAGGGGCTTACCTTAAGAC 4966
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Db 4967 ACAGAGGTTCCCGCTGCGAGAGACCATGAGATTCCTGAGAGAGGCTCTTACAGGCT 5026
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QY 3600 GTATAGGCTGGAGCCGTTCAAAAGGATTTACTACACACAGCCCATACCAATATACAT 3659
Db 5207 GTATAGGCTGGAGCCGTTCAAAAGGATTTACTACACACAGCCCATACCAATATACAT 5266
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QY 3720 AGCTTACAGCTGTGGCGGCTATGCTGCAACAGAGGAGGCTGCTTGTGGGAG 3779
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QY 3780 GATCATCTTGTCCGAGAGGCGGACCATCATTCGAGAGGAGATCTTTACCGGAGATT 3839
Db 5387 GATCATCTTGTCCGAGAGGCGGACCATCATTCGAGAGGAGATCTTTACCGGAGATT 5446
QY 3840 CGATAGATGGAAGAGTGCCTCAGACACCTCCTTATATGAGAGAGGAGATGAGCTCGC 3899
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QY 4020 GTGGAATTTCAACAGCGGATATCAATATTTAGAGGCTTGTGCACTGTGCTGAGACCC 4079
Db 5627 GTGGAATTTCAACAGCGGATATCAATATTTAGAGGCTTGTGCACTGTGCTGAGACCC 5686
QY 4080 CGCGATAGCATCTGATGAGCATTCACAGCTCTATACACAGCCGCTCACACCCACACA 4139
Db 5687 CGCGATAGCATCTGATGAGCATTCACAGCTCTATACACAGCCGCTCACACCCACACA 5746
QY 4140 TACGCTCGGTTTACATCTGAGGAGGATGAGTGGGCGCCCAATTTCTCTCCAGAGCG 4199
Db 5747 TACGCTCGGTTTACATCTGAGGAGGATGAGTGGGCGCTGCTGCCAATGCCGCCCGCAGCG 5806
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QY	4200	TGCTTTCGCTTTCGTAGAGCGCGGCATTCGCTGAGCGGCTGTTGGCAGCATAGGCTTTGG	4259
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QY	4260	GAAGGTGCTTGGATATTTTGGCAGGTTATGGACAGGGGTGGACAGCGCGCTCGTGGG	4319
Db	5867	GAAGGTGCTTGGACATTTTCGGCGGTTATGGACAGGAGTGGCGCGCGCTCGTGGG	5926
QY	4320	CTTTAAGTTCATGAGCGCGAGATGCGCTCCACCGAGAGCTGAGCTAACCTTCCCTGC	4379
Db	5927	CTTTAAGTTCATGAGCGCGAGATGCGCTCCACCGAGAGCTGAGCTAACCTTCCCTGC	5986
QY	4380	TATCCTTCGCCCTGGCGCCAGTCGTGCGGGGTGTGTGGCGCGCATCTGGTGGGCA	4439
Db	5987	CATCCTCTCTCTGGCGCCAGTCGTGCGGGGTGTGTGGCGCGCATCTGGTGGGCA	6046
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QY	4500	GGGTAAACACGTCCTCCCGCAGCATATGTCCTTGAGAGGAGCGCTGACAGAGTGTAC	4559
Db	6107	GGGTAAATCATGTTTCCCGCAGCATATGTCCTTGAGAGGAGCGCTGACAGAGTGTAC	6166
QY	4560	TGAGATCTCTCTAGTCTTACCATCTACTCAGCTGCTGAGAGGCTTGACACAGTATCAA	4619
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QY	4620	CGAGGACGTCTCCAGGCCATGCTCGGCTCGTGGCTTAAGAGATTTGGGATTTGATATG	4679
Db	6227	TGAAGACGTCTCCAGCGGTGTCCGGCTCGTGGCTTAAGAGATTTGGGATTTGATATG	6286
QY	4680	CACGGTGTGACTATTTTCAAGACCTGAGTCTCAGTCAAGCTCTCGCGGATGTCGGG	4739
Db	6287	CACGGTGTGACTATTTTCAAGACCTGAGTCTCAGTCAAGCTCTCGCGGATGTCGGG	6346
QY	4740	AGTCCCTTCTTTCATGTCAAAGTGTGACAGGAGTCTGGCGGGCGACGCGCATAT	4799
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QY	4800	GGAACACACCTGCGCATGTGGAGCAGACATCACCGGACATGTGAAAAAGATTCCATGAG	4859
Db	6407	GGAACACACCTGCGCATGTGGAGCAGACATCACCGGACATGTGAAAAAGATTCCATGAG	6466
QY	4860	GATCGTGGGCTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAAGCGCTA	4919
Db	6467	GATCGTGGGCTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAAGCGCTA	6526
QY	4920	CACACAGGCGCCCTGACAGCCCTCCCGGGCGCAATTATCTAGGGGCTGTGGCGGCT	4979
Db	6527	CACACAGGCGCCCTGACAGCCCTCCCGGGCGCAATTATCTAGGGGCTGTGGCGGCT	6586
QY	4980	GGCTGCTGAGAGTACGTGAGAGTTCAGCGGGGTGGGGATTTCACATACGTAGAGGCAT	5039
Db	6587	GGCGGTGAGAGTACGTGAGAGTTCAGCGGGGTGGGGATTTCACATACGTAGAGGCAT	6646
QY	5040	GACACATGACACGTAAAGTGGCGGTGTACAGTTCCGCGCCCGCGAATTTCCACAGAGT	5099
Db	6647	GACACATGACACGTAAAGTGGCGGTGTACAGTTCCGCGGTGTACAGTTCCGCGAGT	6706
QY	5100	GGATGGGGGCGGTTGACAGGTAGCTCCACGCTGCAAAACCCCTCTACGAGGAGAGT	5159
Db	6707	GGAGGAGTGGCGTTTACAGGTAGCTCCGCGGTGTACAGGCTTCTCTTAAGGAGAGT	6766
QY	5160	CACATCTCTGTTGCGGCTCAATCAATACCTGTTGGTCAACAGCTCCATCGAGCCGA	5219
Db	6767	TACATTCAGGTGGGCTCAACCAATACCTGTTGGTCAACAGCTCCATCGAGCCGA	6826
QY	5220	ACCGGAGAGTACGAGTCTACATTCATGCTACGACCGCCCTCCCATTAAGCGGAGAC	5279
Db	6827	ACCGGAGTACGAGTCTACATTCATGCTACGACCGCCCTCCCATTAAGCGGAGAC	6886
QY	5280	GAGTAAAGCTAGGCTGCGCAGGGGATCTCCCGCTCTTGGCAGCATCATAGCTAGCA	5339

Db	6887	GGCTAAGCGTAAAGTTGGCCAGG66GCTCTCCCTCTCTTGGCCAGCTCTTACAGTACCC	6946
OY	5340	GCATGTGGCCCTTCCTTGAAGGCAATGCACTACCCGTCATGACTTCCCGGACGCTGA	5399
Db	6947	GTTGTCTGGCCCTTCCTTGAAGGCAATGCACTACCCAGCATCTCTCTCGGACGCTGA	7006
OY	5400	CCATCATCGAGCCCAACCTCTTGGCGGCAAGAGATGGGGGGGAAACATCAACCCGCTGA	5459
Db	7007	CTCATCTAGAGGCCAACCTCTTGTGGCGCAAGAGATGGGGGGGAAACATCAACCCGCTGA	7066
OY	5460	GTCAGAAATAAGATAGTAAATTTTGGACTCTTTCGAGGCCGCTCCAGCCGAGAGAGATGA	5519
Db	7067	GTCGAGAAACAAGATAGTAAATTTTGGACTCTTTCGAGGCCGCTCCAGCCGAGAGATGA	7126
OY	5520	GAGGGAAGTATCCGTTCCGGCGGAGATCCTGGGAGGTCCAGGAAATTCCTCGAGGAT	5579
Db	7127	GAGGGAAGTATCCGTTCCGGCGGAGATCCTGGGAAATTCAGGAAATTCCTCGAGGAT	7186
OY	5580	GCCCATATGAGGACGCGCCGATATACACCTTCACCTTTAAGTCTTGAGAGAGACCGGA	5639
Db	7187	GCCCATATGAGGACGCGCCGATATACACCTTCACCTTTAAGTCTTGAGAGAGACCGGA	7246
OY	5640	CTACGTCCTCCAGTGTACACGGGTGTCCATATGCCGCTGCGCAAGGCCCTCCGATAC	5699
Db	7247	CTACGTCCTCCAGTGTACACGGGTGTCCATATGCCGCTGCGCAAGGCCCTCCGATAC	7306
OY	5700	ACCMCCACGAGGAAGAGAGAGGATGTGCTGTGCACAATCTACCGTGTCTTTCGCTTGGC	5759
Db	7307	ACCTCCACGAGGAAGAGAGAGGATGTGCTGTGCACAATCTACCGTGTCTTTCGCTTGGC	7366
OY	5760	GGAAGCTGCCCACAAAGACCTTCGGGACGCTCGAATGTGCGCGGTGCAAGCGCACGCG	5819
Db	7367	GGAAGCTGCGACTAAAGACCTTCGGGACGCTCGAATGTGCGCGGTGCAAGCGCACGCG	7426
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Db	7427	GAGCGCTTCTTCGACCAAGGCTCTCGAGACAGCGGTGACAAAGAGATCCGAGCTTGAGTGTGA	7486
OY	5880	CTCTCCATGACCCCTTGAAGGGAGGAGCGGGGAGATCCCGATCTCAAGCAAGGCTCTTG	5939
Db	7487	CTCTCCATGACCCCTTGAAGGGAGGAGCGGGGAGATCCCGATCTCAAGCAAGGCTCTTG	7546
OY	5940	GTCACGCTAAGGAGAGAGCTAGTAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5999
Db	7547	GTCACGCTAAGGAGAGAGCTAGTAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	7606
OY	6000	GACAGGCGCCCTATACAGGCATGCGCTCGGAGAGAAACAAGCTGCCATCAATGCACT	6059
Db	7607	GACAGGCGCCCTATACAGGCATGCGCTCGGAGAGAAACAAGCTGCCATCAATGCACT	7666
OY	6060	GAGCAACTTCTTGTCTCGCTGACACACACTTGGTCTATGCTAAACAATGTCGAGGCAAG	6119
Db	7667	GAGCAACTTCTTGTCTCGCTGACACACACTTGGTCTATGCTAAACAATGTCGAGGCAAG	7726
OY	6120	CCTCGGCAAGAGAGTCACTTATGACAGACTGCAAGTCTCTGAGAGCAACACTACCGGA	6179
Db	7727	CCTCGGCAAGAGAGTCACTTATGACAGACTGCAAGTCTCTGAGAGCAACACTACCGGA	7786
OY	6180	CGTGTCTCAAGAGATGAAGCGAGGCGTCCACAGTTAAGCTTAACTTCTATCCGTGGA	6239
Db	7787	CGTGTCTCAAGAGATGAAGCGAGGCGTCCACAGTTAAGCTTAACTTCTATCCGTGGA	7846
OY	6240	GGAAGCCGTAAGTGTGAGCGCCCAATTCGCGCAATTAATTTGGCTATGAGGGCAAA	6299
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OY	6300	GGAAGCTCCGGAACCTATCCAGCAAGGCGGTTAAACAACATCGCTCCGTGTGGAAGACTT	6359
Db	7907	GGAAGCTCCGGAACCTATCCAGCAAGGCGGTTAAACAACATCGCTCCGTGTGGAAGACTT	7966
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D	7967	GCTGAAGACACTGTACACACCAATTGACACACCAATCATGGCAAAAATGAGTTTCTG	8026
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D	8027	TGTCCAACCCAGAGAGAGAGGGCGGTAAAGCACCCGCCCTTATCGTATTCCAGATTGGG	8086
Q	6480	GGTTCGCTGTGGAGAGAAATGGCCCTTTACGATGAGGCTCCACCTCCCTCAAGCGCT	6539
D	8087	AGTCGCTGTATGGAGAGAGATGGCCCTCTATGATGTGGTCTCCACCTCCCTCAAGCGCT	8146
Q	6540	GATGGGCTCTTCATACGATTCCAATACTCTCTGTGGACAGGGGGTGGAGTTCTGTGAA	6599
D	8147	GATGGGCTCTCTACGAGATTCCAGTACACTCTCTGGGGCAGGAGTCGATCTGGTAA	8206
Q	6600	TGCGTGAAGAGCAAGAAATGGCCCTTATGGGCTTCGATATGACACCCGCTTTTGGTGC	6659
D	8207	TACTCGAATATCAAGAGAAACCCCAATGGGCTTTCTATATGACATCGCTGTGTGATGC	8266
Q	6660	AACGCTACTAGATATGACATCCGCTTTTGAAGAGTCAATCTCCCAATTTTGACTTGGC	6719
D	8287	AAGGCTACCCGAGAGAGACATCCGTGTGAGGAGTCAATTTCACATGTGTGACTTGGC	8326
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D	8327	CCCCGAAAGCCAGACAGGCCATAAATCGCTCAGACAGCGGCTTTATATCGGGGGCCCT	8386
Q	6780	GACTAATTTAAAGGGCAGAGACTGCGGCTATGCGCGCTCGCGGAGGGGTGACTGAC	6839
D	8387	GACTAATTTCAAAAGGGCAGAGACTGCGGCTTATCGCGGCTCGCGCGAGGCGCTGTAC	8446
Q	6840	GACCAGCTCGGCTAATACCTCTACATGTTACTTGAAGCGCGCTCGGCTGTGAGCTGC	6899
D	8447	GACTAGCTGGGGTAACACCTCTACATGTTACTTGAAGCGCGCTGTGAGCTGTGCG	8506
Q	6900	GAACTCTCAGAGACTGCACGATGCTGCTATGCGGAGAGACACTTGTGCTATGTGGAAG	6959
D	8507	GAACTCTCAGAGACTGCACGATGCTGCTGGAAGGAGAGACACTTGTGCTATGTGGAAG	8566
Q	6960	CGCGGGAGCCCAAGAGAGACAGCGGACTTACGCGGCTTCAAGGAGCTATGACTAGTA	7019
D	8567	CGCGGGAGCCCAAGAGAGACCGGGGAGGCTTACGAGCTTCAAGGAGCTATGACTAGSTA	8626
Q	7020	CTTGGCCCCCTTGGGAGCCCCGCCCAACACAGATACGACTTGGATGATTAACATCAG	7079
D	8627	CTTGGCCCCCTTGGGAGCCCCGCCCAACACAGATACGACTTGGATGATTAACATCAGT	8686
Q	7080	CTCTCCCAATGTGTACATGCTCGGACGATGATGTGCAAAAAGGTTACTATCTACCGG	7139
D	8687	TTCTCTCCCAATGTGTGCGGTGCGCCACGATGATGAGGCAAAAAGGTTACTATCTACCGG	8746
Q	7140	TGACCCCAACACCCCCCTTGGCGGGGCTGCTGTGGAGACGCTAGACACTTCCAGTCAA	7199
D	8747	TGATCCCAACACCCCCCTTACGACGGGCTGCTGTGGAGAGACGCTAGACACTTCCAGTCAA	8806
Q	7200	TTCCTGGGTAGCAACATCATCATGTATGCGCCACCTTGTGGGCAAGGATATCTCAT	7259
D	8807	CTTCGCGCTAGGCAACATTAATATGATGTGGGCCACTTGTGTGGCAAGGATATCTCAT	8866
Q	7260	GACTCATTTCTTCCATCCCTTCTAGCTCAGAACACTTGAANAAGCCCTAGATTGTCA	7319
D	8867	GACTCATTTCTTCCATCCCTTCTAGCGGACAGAACACTTGAANAAGCCCTAGATTGTCCA	8926
Q	7320	GATCTAGGGGGCGTATACATCATGTCGACACTTGCACATCCGACATATTCACAGACT	7379
D	8927	GATCTAGGGGGCGTATACATCATGTCGACACTTGCACATCCGACATATTCACAGACT	8986
Q	7380	CCATGGCCCTTAGCCATTTTCTACTCTCATTTACTCTCCAGGTGAGATCAATAGGTGGC	7439
D	8987	CCATGGCCCTTAGCCATTTTCTACTCTCATTTACTCTCCAGGTGAGATCAATAGGTGGC	9046
Q	7440	TTTCATGCTCAGAAACTTGGGGTACGGCCCTTGGCAGTCTGGAGACATCGGGCCAGAG	7499
D	9047	TTTCATGCTCAGAAACTTGGGGTACACCCCTTGGCAGTCTGGAGACATCGGGCCAGAG	9106

QY	7500	TGTCGGGGCTAGAGCTATGTCGCCAGGGGGGAGAGGCTGCGACTTGTGGCAAGTACTCTT	7559
Db	9107	CGTCGGGGCTAGAGCTATGTCGCCAGGGGGGAGAGGCTGCGACTTGTGGCAAGTACTCTT	9166
QY	7560	CAACTGGGCGAGTAGAGACCAAGCTCAACTCACTCCCAATCCCGGCTGGCTCCAGTTGGA	7619
Db	9167	CAACTGGGCGAGTAGAGACCAAGCTCAACTCACTCCCAATCCCGGCTGGCTCCAGTTGGA	9266
QY	7620	TTTATCCAGCTGGTTCGCTTCTCTGCTTACACAGGGGGGAGACATATATACAGCTCTCG	7679
Db	9227	CTTGTCCGGGCTGGTTCGCTTCTCTGCTTACACAGGGGGGAGACATATATACAGCTCTCG	9286
QY	7680	TGCCGACCCCGGCTGATTCATGTGAGCCCTACTCTACTTTCTGTAGGGGTAGGACATGA	7739
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QY	7740	TCTACTCCCAACCGATGAGACGGGAGACTAAACATCCAGGCCATATGCTCTCT	7799
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QY	7800	TTTTCCTCTT 7809	
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RESULT 9			
US-09-315-850-1			
: Sequence 1, Application US/09315850			
: Patent No. 6217872			
: GENERAL INFORMATION:			
: APPLICANT: OKAYAMA, Hiroto			
: APPLICANT: FUKU, Isao			
: APPLICANT: MORI, Chisato			
: APPLICANT: TAKAMIZAWA, Akahisa			
: APPLICANT: YOSHIDA, Iwao			
: TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC			
: TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE			
: NUMBER OF SEQUENCES: 50			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &			
: ADDRESSEE: Naughton			
: STREET: 1725 K St. N.W. Suite 1000			
: CITY: Washington			
: STATE: D.C.			
: COUNTRY: U.S.A.			
: ZIP: 20006			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Diskette, 3.5 in, 1.44mb			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0			
: SOFTWARE: ASCII			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/09/315,850			
: FILING DATE:			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US/08/904,686			
: FILING DATE: 01-AUG-1997			
: APPLICATION NUMBER: US 08/324,977			
: FILING DATE: 18-OCT-1994			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: JP 2-167466			
: FILING DATE: 25-JUN-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: JP 2-230921			
: FILING DATE: 31-AUG-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: JP 2-305605			
: FILING DATE: 09-NOV-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: US 08/099,706			
: FILING DATE: 30-JUL-1993			
: PRIOR APPLICATION DATA:			

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1      APPLICATION NUMBER: US 07/769,996
2      FILING DATE: 02-OCT-1991
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US 07/635,451
5      FILING DATE: 28-DEC-1990
6      ATTORNEY/AGENT INFORMATION:
7      NAME: McLeand, Le-Nhung
8      REGISTRATION NUMBER: 31,541
9      REFERENCE/DOCKET NUMBER: 900703G
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: (202) 659-2930
12     TELEFAX: (202) 887-0357
13     INFORMATION FOR SEQ ID NO: 1:
14     SEQUENCE CHARACTERISTICS:
15     LENGTH: 9416 base pairs
16     TYPE: nucleic acid
17     STRANDEDNESS: single
18     TOPOLOGY: linear
19     MOLECULE TYPE: cDNA from genomic RNA
20     FEATURE:
21     NAME/KEY: CDS
22     LOCATION: 353..9362
23     US-09-315-850-1

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Query Match	65.3%	Score 5218:	DB 4:	Length 9416:
Best Local Similarity	91.8%	Pred. No. 0:		
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			Gaps	0:
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Db 3407	CCTGGCCGCCCATCACGGCTACTCCCAACAGACGGCGGCCCTACTTGGTGCATCATCAC	3466		
QY 1860	TAGCCTACAGGGCCGGAGACAGACAGGTTCAGGGGAGAGTTCACGGTGGTCTCACCCG	1919		
Db 3467	TAGCCTTACAGGCCGGGGACAGACAGCAGGTTCAGGGAGAGTTCAGGTGGTTCACCCG	3526		
QY 1920	AACCAATCTTTCCTGGCGACCTGGGTCAATGGCGTGTGTGACGTCTATCATGTGGTC	1979		
Db 3527	AACCAATCTTTCCTGGCGACCTGGGTCAACGGCGTGTGTGACCGTTCATCATGTGGTC	3586		
QY 1980	CGGTCACAAACCCCTTGGCGGCCCAAGGGGCCCATTCACCCAAATGTACACCAATGTGA	2039		
Db 3587	TGGCTCAAAAGCCTTACCGCGCGCAAGGGGCCCATTCACCCAGATGTACATATGTGA	3646		
QY 2040	CCAGACCTGTGTGGCTGGCCAGCGCCCGCGGGCGCTTCTTGAACCATGTACACTG	2099		
Db 3647	CCAGACCTGTGTGGCTGGCCAGCGCCCGCGGGCGCTTCTTGAACCATGTACACTG	3706		
QY 2100	CGGAGCTCGGACCTTACTTGGTTCACGAGGATCGCATGTCCATTCGGGTGGCGCGGCG	2159		
Db 3707	TGGAGCTCAGACCTTACTTGGTTCACGAGATGTGTACGTCAATTCGGGTGGCGCGGCG	3766		
QY 2160	GGGCGACAGAGGGGGAGACCTACTCTCCCGAGGCCCTCTCTACTTGAAGGGCTTTC	2219		
Db 3767	GGGCGACAGTGAAGGGGGAGCCTGCTCTCCCGAGGCCCTCTCTACTTGAAGGGCTTTC	3826		
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Db 3827	GGGGGTGTCACTGCTGGCCCTGGGGGAGACCTGTGGGCAATCTTGGGGTGGCGGTG	3886		
QY 2280	CACCCGAGGGGTTGCGAAGCGGTGACCTTTTACCCGTCGACGTATATGAACCACTAT	2339		
Db 3887	CACCCGAGGGGTTGCGAAGCGGTGACCTTTTGGGCCCGTAGAGTCAATGAACCACTAT	3946		
QY 2340	GGGGTCCCCGCTTTCACGACACTGTGCCCTCCGGCCGTACCGCAGATATCCAGGT	2399		
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QY 2400	GAGCATCTACACGCCCTACTGTTAGCGGCAAGACACTAAGTGGCGGCTGGGTATGC	2459		
Db 4007	GGCCCACTTACAGCGCTCCCACTGGACGGCGCAAGATACTAAGTGGCGGCTGGATATGC	4066		
QY 2460	AGCCCAAGGTAATAGGTGTTGTCTCTGAACCGTTCGTGGCCCGCACCTAGTATTGCG	2519		

D	b	4067	AGCCCAAGGGATACAAAGTGTGTCCTCATATCCGTCCTCGTTGGCCGCTACTCTTAAGSGTTTG	4126
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D	b	4127	GGCCTAATGTCTTAAGGCACAGGATTATACCCCAACATCAAGAACTGGGGTAAGSACAT	4186
O	y	2580	CACCAAGGCGGCCCATCACAGTACTCCACCTATGGCAAGTTCTTTGCCAGCGGTGTG	2639
D	b	4187	TACCACAAGCGCCCCGTCATACACTCTACCTATGGCAAGTTCTTTGCCAGTGTG	4246
O	y	2640	CTCTGGGGGGCCTTAGTACATCATAATATGTATAGTGGCCATCACTGACTGCACAC	2699
D	b	4247	CTCTGGGGGGCCTTAGTACATCATAATATGTATAGTGGCCATCACTGACTGCATAC	4306
O	y	2700	TATCCTGGGCGATCGGCACAGTCTCTGGACCCAGAAGCGCTGGAGCGCGACTGTGCT	2759
D	b	4307	AATCTTGGGCGATCGGCACAGTCTCTGGACCCAGAAGCGCTGGAGCGCGCTGTGCT	4366
O	y	2760	GCTGGCCACCGGATACGGCTCCGGGATCGGTACACCGGCCACATCCAACTCGAGAGGT	2819
D	b	4367	GCTGGCCACCGGATACGGCTCCGGGATCGGTACACCGGCCACCAACTCGAGAGGT	4426
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D	b	4427	GGCCCTGTCTAATACTGGAGAGATCCCCCTTTATGGCAAAGCCATCCCATCGAACCAT	4486
O	y	2880	CAAGGGGGGGGAGGACCTCAATTTTCGCATTCGAAGAAGAA ^Δ TGTATGAGTGCGGCG	2939
D	b	4487	CAGGGGGGGAAGGATCTCATTTTCTGTCTTCATTCGAAGAAGAA ^Δ TGTATGAGTGCGGCG	4546
O	y	2940	GAACTGTCCGGECTCGGACTCAATGCTGTASCATTTACGGGGCCTTATATCCGT	2999
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D	b	4607	CATACCACTATGCGGAGACGTCTGTGTGCGGCAACAGACGCTGTGATGAGCGGCTATAC	4666
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D	b	4667	GGGGCACTTTCGACATGATGCATGATGCATATATATGTCTACCCAGACAGTGTGACTTAG	4726
O	y	3120	CCTGAGCCCGACCTTTCACCAATTGAGAGCAGACCGCTGCCACAAGACGGGTGCACGCTC	3179
D	b	4727	CTTGATCCCACTTTCACCAATTGAGAGCAGACCGCTGCCACAAGACGGGTGCACGCTC	4786
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D	b	4847	AGAAAGGCGCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGATGCTATAGCGGGGCT	4906
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D	b	4907	TGCTTGTACAGATCAACGCCCGCGGAGACTCAGTTAGTTGCGGGGTTTACTCTAAACAC	4966
O	y	3360	ACCAAGGTTGGCCCTTCGCCAGAGACATCTGAGATTCTGGAGAGCGCTTTTACAGGCT	3419
D	b	4967	ACCAAGGTTGGCCCTTCGCCAGAGACATCTGAGATTCTGGAGAGCGCTTTTACAGGCT	5026
O	y	3420	CACCCACATTAACGCCCATTTCTTTGCCAGACTAATAGCAGGACGAGAAATCTCCCTA	3479
D	b	5027	CACCCATTAATATGATGACATCTTTCTTTGCCAGACCAAGCAGGAGGAGAAATCTCCCTA	5086
O	y	3480	CCTGTATACATACAGGCTACAGGTGTGTGCCAGAGGCTCAGGGCTCACCTCATCTGTGGA	3539
D	b	5087	CCTGTATACATACCAAGCAAGGTGTGTGCCAGAGGCTCAGGGCCCACTCTCATCTGTGGA	5146
O	y	3540	CCAATGTGGAAGTGTCTCATACGCGCTAAGCTACGCTGACACGGGCGCAAGCCCTCTCT	3599

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Db 5207 GTACAGGCTGGAGCCGCCAGAAATGAGGTCCACCCCTCACCCACCCCAATAACAAATACAT 5266
Qy 3660 CATGACATGATGCGGCTGACCTGGAGAGTGTGTGACAGAGACCCGGGTGTGTAGGGG 3719
Db 5267 CATGACATGATGCTGGCTGACCTGGAGAGTGTGTGACAGAGACCCGGGTGTGTAGGGG 5326
Qy 3720 AGTCTAGACAGCTGTGGCCGCGTATTCCTGACACAGCAGCGTGTGCTCATTTGTGGAGC 3779
Db 5327 AGTCTTAGAGCTGTGGCCGCGTATTCCTGACACAGCAGCGTGTGCTCATTTGTGGAGT 5386
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Db 5447 CGATGAATGGAAGAGTCCGCTCGCACTCCCTACATGAGAGGGAATGACGTCCG 5506
Qy 3900 CGAACAATTCAAACGAGGCAATCGGTTGCTGCAAAACGCCACACAGCAAGCGAGCG 3959
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Db 5867 GAAGTGCTTGTGATATTTTGGCAGGTTATGAGCAGGGGATGGCAGCGCTCGTGGC 5926
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Db 5927 CTTTAAGGTCATGAGCGGCGAGATGCCCTCCACGAGGAGCTGGCTACTACTCTCTGG 5986
Qy 4380 TATCTCTCCCTGCGCGCCCTAGTGTGCGGGGTGCTGCGCAGCGATCTGCTGCGCA 4439
Db 5987 CATCTCTCTCTGCGCGCCCTAGTGTGCGGGGTGCTGCGCAGCAATACTGCTGCGCA 6046
Qy 4440 CGTGGGCCAGGAGGGGGGTGTGCACTGAGTAAACCGGCTGATACCGTTCGCTCGCG 4499
Db 6047 CGTGGGTCCGGAGAGGGGGGTGTGCACTGAGTAAACCGGCTGATACCGTTCGCTCGCG 6106
Qy 4500 GGGTAAACAGCTTCCCCACGACACTATGTGCTGAGAGGAGAGCTGACAGAGTGTGAC 4559
Db 6107 GGGTAAATCATGTTTCCCCACGACACTATGTGCTGAGAGGAGAGCGCGGTGTAC 6166
Qy 4560 TTAGATCTCTCTAGTCTTACCATCACTCAAGTGTGCTGAAAGGCTTACCAAGTGTGCA 4619
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Qy 4620 CGAGACTGTCTACAGGCGCATCGCGCTGTGCTAAGAGATGTTGGATGGATGAT 4679
Db 6227 TGAACACTGCTCACACCGGTGTTCGGGCTGTGCTAAGGATGTTGGAGACTGGATATG 6286

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Db 6347 AGTCCCTTCTTCATGATGACCTGGGTACAAAGGAGTGTGGCGGGGACAGGATCAT 6406
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Db 6407 GCAACCACTGCTCCCATGTGGAGCAGACATCACCGCATGTGAAAAAGGTTCCATGAG 6466
Qy 4860 GATCTGGGGCTGAGACCTGTACTAAGCTGGCATGGAACATTCCTCCATTAACCGTA 4919
Db 6467 GATCTGGGGCTGAGACCTGTACTAAGCTGGCATGGAACATTCCTCCATTAACCGTA 6526
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Db 6707 GGACGAGTGGGTTGCAAGAGTACGCTCCAGGCTGCAAAACCCCTCTACGAGAGAGT 6766
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Qy 5220 ACCGAGCTACAGTGTCTCACTTCCATGCTCACCGACCCCTCCACATTTACGGGAGAC 5279
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Qy 5280 GAGTAAAGCTAGGCTGGGCGAGGAGTATCCCGCTCTTGGAGAGCTACATCACTGAGCA 5339
Db 6887 GAGTAAAGCTAGGCTGGGCGAGGAGTATCCCGCTCTTGGAGAGCTACATCACTGAGCA 6396
Qy 5340 GCTGTCTGCGCTTCTTGAAGGCAACATGCACTACCGTGTACTCCCGGAGCGCTGA 5399
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Qy 5580 GCCCATATGGGACGCGCGGATTAACAACCTCCATCTTGAAGTCTGGAAGGACCCGGA 5639
Db 7187 GCCCATATGGGACGCGCGGATTAACAACCTCCATCTTGAAGTCTGGAAGGACCCGGA 7246
Qy 5640 CTACGTCCTCCAGTGTGACGCGGGGTGTCATTTCCCGCCCGCAAGGCGCCCTCCGATAC 5699
Db 7247 CTACGTCCTCCAGTGTGACGCGGGGTGTCATTTCCCGCCCGCAAGGCGCCCTCCGATAC 7306
Qy 5700 ACCCTCACGAGAGAGAGAGAGGTTGTCTGTGCAAGTATCAAGGATGTCTTCTGCTGAG 5759
Db 7307 ACCCTCACGAGAGAGAGAGAGGTTGTCTGTGCAAGTATCAAGGATGTCTTCTGCTGAG 7366

QY	5760	GGAGAGCTGGCCAAACAAACCTTGGGAGCTCCGCAATCTGTCGGCCGTCACACGGCCAGGC	5819
Db	7367	GGAGACTGCTACTAATAACCTTTGGGAGCTTCCGCAATCTGTCGGCCGTCACACGGCCAGGC	7426
QY	5820	AACGGCTCTCTCTGACCAAGCCCTCCGAGCAGCGGCCAGCGGGATCCAGCTTGAGTGGTA	5879
Db	7427	GACCGCCCTTCTCGACCAAGCCCTCCGAGCAGCGGGATCCAGCAAGATCCAGCTTGAGTGGTA	7486
QY	5880	CTCTCCATGCCCCCTTGGAGGGAGCGCGGGGATCCCGATCTCAGCAGCGAGTCTTG	5939
Db	7487	CTCTCCATGCCCCCTTGGAGGGAGAACCGGGGGACCCCGATCTCAGATGACGGGTCTTG	7546
QY	5540	GTCTACCGTAAGCGAGGAGGCTAAGTGAAGACGTCTGTGTGCTCGATGTCTTACATAG	5999
Db	7547	GTCTACCGTAAAGGAGGAGGCTAAGTGAAGATGTGTGTGCTCGATGTCTTACATAGT	7606
QY	6000	GACAGCGCCCTTATACGCCATGCGCTCCGGAGAGAAACAAGCTGCCCATCAATGAGACT	6059
Db	7607	GACAGCGCCCTTATACGCCATGCGCTCCGGAGAGAAACAAGCTGCCCATCAAGCGTT	7666
QY	6060	GAGCAACTCTTGTCTCCGCTACCAACAATTGGTCTATGTGTACAAATCTCGCAGCGAAG	6119
Db	7667	GAGCAACTCTTGTCTCCGCTACCAACAATTGGTCTATGTGTACAAATCTCGCAGCGAG	7726
QY	6120	CTTCGCGCAAAAGAGTGAACCTTTGACAGACTGAGAGTCTCGAGCAGCACTACCGGA	6179
Db	7727	CTTCGCGCAGAAAGAGTGAACCTTTGACAGACTGGAAGTCTCGAGCAGCACTACCGGGA	7786
QY	6180	CGTGTCTCAAGAGATGAAGGCCAAGGCTTCACAGTGAAGGCTAACTTCTATCCGTGGA	6239
Db	7787	CGTGTCTCAAGAGATGAAGGCCAAGGCTTCACAGTGAAGGCTAACTTCTATCCGTATGA	7846
QY	6240	GGAAGCCTGTAACTGACGCGCCCACTTCGCGCAAGTCTAAATTTGGCTATGGGCAAA	6299
Db	7847	GGAAGCCTGTAACTGACGCGCCCACTTCGCGCAATCAAGTTTGGCTATGGGCAAA	7966
QY	6300	GGAGCTGCCGAACCTTACAGCAAGGCGCTTAAACAATCCGCTCCGCTGGAAGACTT	6359
Db	7907	GGAGCTGCCGAACCTTACAGCAAGGCGCTTAAACAATCCGCTCCGCTGGAAGACTT	7966
QY	6360	GCTGGAAGACACTGAGACACCAATTATACACACCAATCATGSCAAAAAATGAGTTTCTG	6419
Db	7967	GCTGGAAGACACTGAGACACCAATTATACACACCAATCATGSCAAAAAATGAGTTTCTG	8026
QY	6420	CGTCCACACGAGAAGGGGGGGCGGCAAGCAGTGGCTTATGATTTCCAGATTGSG	6479
Db	8027	TGTCCAAACCGAAGAAAGGAGGCGGTAAAGCAGCGCCCTTATGATTTCCAGATTGSG	8086
QY	6480	GGTTCGTGTGGGAGAAAAATGGCCCTTTACGATGTGTCTCCACCTCTCCAGGCGGT	6539
Db	8087	AGTCCGTGTGTGGGAGAAATGGCCCTTTATGATGTGTCTCCACCTCTCCAGGCTGT	8146
QY	6540	GATGGGCTCTTAATAGGATTTCCAAATACACTCTCTGAGCAGGGGCGAGTTCTGTGAA	6599
Db	8147	GATGGGCTCTCTAATAGGATTTCCAGTACTCTCTGAGCAGGAGTGTGAAATCTGTGTA	8266
QY	6600	TGCGTGAAGACGAAGAAATGCCATATGGGCTTCGATATGACACCCTGCTTTTGACTC	6659
Db	8207	TACCTGGAATTCAAAGAAAAACCCCATGGGCTTTCTATATGACACTCGTGTGTTGACTC	8266
QY	6660	AACGGTACAGAGATATACATCCGCTGTGAGAGGTCAATCTCCATGTGTGGAATTGCG	6719
Db	8267	AACGGTACCGAGACACATCCGCTGTGAGAGTCAATTTACCATGTGTGGAATTGCG	8326
QY	6720	CCCCGAGCCAGACAGCCATTAAGTGCTCACAGGCGGCTTTACATGGGGGCCCTT	6779
Db	8327	CCCCGAGCCAGACAGCCATTAATAATGCTCACAGGCGGCTTTATGCGGGGGCTCTT	8386
QY	6780	GACTAATTCTAAAGGAGAGACTGCGGCTTTCGCGGTACCGGCGAGGCGGTCTACTAC	6839
Db	8387	GACTAATTCTAAAGGAGAGACTGCGGTTATGCGCGGTACCGGCGAGGCGGTCTCTAC	8446
QY	6840	GACCAAGCTGCGGTATATCCCTCACATGTTACTTGAAGGCCCTGCGGCTGTGCAGACTGC	6899

D	8447	GACTAGCTGGGTAACACCCTGCATGTAAGGAGGCTCTGCAGGCTTCGACGCTTC	8506
Q	6900	GAAAGCTCGAGGACTGCACGATGCTGCTATGCGGAGACAGACTTTCGTTATCTGTGAAG	6959
D	8507	GAAAGCTCGAGGACTGCACGATGCTGCTATGCGGAGAGAGCAGCTTCGTTATCTGTGAAG	8566
Q	6960	CGCGGGAGCCCAAGAGAGACGAGGCGAGGCTTACGAGGCGCTTACAGGAGGCTATGACTAGATA	7019
D	8567	CGCGGGAGCCCAAGAGAGAGAGGAGCCGAGGAGCTTACGAGGCTTACAGGAGGCTATGACTAGATA	8622
Q	7020	CTCTGCCCCCCTCTGGGGAGCCGCCCAACCGAGATTCGACTTGGAGTTGATATCATG	7079
D	8627	CTCTGCCCCCCTCTGGGGAGCCGCCCAACCGAGATTCGACTTGGAGTTGATATCATG	8686
Q	7080	CTCTGCAATGTGTGAGTGGCGGAGATGATGTGGCAAGAGGATTAATCATACCG	7133
D	8687	TTCTCTCAATGTGTGAGTGGCGGAGATGATGTGGCAAGAGGATTAATCATACCG	8748
Q	7140	TGACCCACCAACCCCTTCGCGGGAGCTGCGTGGGAGAGGCTAGACACATCCAGTCAA	7199
D	8747	TGATCCACCAACCCCTTCAGACGAGGAGTGGTGGAGACGATAGACACATCCAGTTAA	8806
Q	7200	TTCTGAGCTAGGACATCATCATATGAGCGCCACCTTGTGGGCAAGATATCTCAT	7255
D	8807	CTCTGAGCTAGGACATCATCATATGAGCGCCACCTTGTGGGCAAGATATCTCAT	8866
Q	7260	GACTCATTTCTTCGCATCTCTTACGTGAGACACTTGAAGAGCCCTAGATTGTCA	7318
D	8867	GACTCATTTCTTCGCATCTCTTACGTGAGACACTTGAAGAGCCCTAGACTGTCA	8922
Q	7320	GATCTACGGGAGCTGTACTCCATGTGAGCCATTGACCTTACCTCAGATCATTCAGAGCT	7378
D	8927	GATCTACGGGAGCTGTACTCCATGTGAGCCATTGACCTTACCTCAGATCATTCAGAGCT	8986
Q	7380	CCATGAGCCTTAGGCACTTTTACATCCATATGTTACTCCAGGAGGATCAATAGGATGAC	7433
D	8967	CCATGAGCCTTAGGCACTTTTACATCCATATGTTACTCCAGGAGGATCAATAGGATGAC	9044
Q	7440	TTTATGCTTCAGGAACTTGGGGTACGCCCTTGCGAGTCTGGAGCATCGGGCCAGAAG	7499
D	9047	TTTATGCTTCAGGAACTTGGGGTACGCCCTTGCGAGTCTGGAGCATCGGGCCAGAAG	9106
Q	7500	TGTCCCGGCTTAGGCTACTGTGCCAGGGGGGAGAGGCTGCACCTTGGGCAAGTACTCTT	7558
D	9107	TGTCCCGGCTTAGGCTACTGTGCCAGGGGGGAGAGGCTGCACCTTGGGCAAGTACTCTT	9166
Q	7560	CAACTGGGCAATGAGACCAAGCTCAAACTCACTCCAAATCCCGGCTCTCCAGTTGA	7619
D	9167	CAACTGGGCAATGAGACCAAGCTCAAACTCACTCCAAATCCCGGCTCTCCAGTTGA	9228
Q	7620	TTTATCAGCTGTTGTTCTGTGCTGTTTACAGCGGGGAGAGCATATATCACAGCTGTCTG	7677
D	9227	TTTATCAGCTGTTGTTCTGTGCTGTTTACAGCGGGGAGAGCATATATCACAGCTGTCTG	9288
Q	7680	TGCCGAGACCCGCTGATTCAATGTGAGGCCATCTCACTTCTGTAGGGGTAGGACATCA	7733
D	9287	TGCCGAGACCCGCTGATTCAATGTGAGGCCATCTCACTTCTGTAGGGGTAGGACATCA	9344
Q	7740	TCTACTCCCAACCGATGAAGGGGAGACTTAACACTCCAGGCCCAATAGGCCATCTCTGTT	7799
D	9347	CTCTGCTCCCAACCGATGAAGGGGAGATTAACACTCCAGGCCCAATAGGCCATCTCTCTT	9406
Q	7800	TTTTTCCCTT 7809	
D	9407	TTTTTTTT 9416	

RESULT 10
US-08-823-895A-27
; Sequence 27, Application US/08823895A
; Patent No. 6433159
; GENERAL INFORMATION:

QY	3300	TGTTGTTAGACACTACGCGCCGCGAGACGCTCAGTTAGTGTGGGGCTTACCTAAACAC	3359
Db	4907	TGCTGTGTAGACACTACCGCGGCGAGACCTGGTTAGTGTGGGGCTTACCTGAACAC	4966
QY	3360	ACGAGGTTGCCGCTGTGCGAGGACCATCTGGAGTTCGGGAGAGCGCTCTTACAGGCTT	3419
Db	4967	ACGAGGTTCCCGTGTGGCCAGGACCACTGGAGTTCGGAGAGTGTCTTCACAGGCTT	5026
QY	3420	CACCCATATGAGAGCCCATTTCTGTGCCAGACTAAGAGGCGAGAGCAACTTCCGCTA	3479
Db	5027	CACCCATATGAGAGCACTTCTGTGCCAGACCAAGAGGCGAGAGCAACTTCCGCTA	5086
QY	3480	CCTGTGATACACAGCTACGCTGTGGCCGAGGCTCAGGCTCCACCTCCATCTGTGGGA	3539
Db	5087	CCTGTGATACCAAGCCAGCGTGTGGCCAGGCTCAGGCTCCACCTCCATCATGTGGGA	5146
QY	3540	CCAAATGGAAGTGTCTCATACGGCTGAAGGCTACGGTGTGAGGGGCAAGGCCCTGCT	3599
Db	5147	TCAAATGTGAAGTGTCTCATACGGCTGAAGGCTACGGTGTGAGGGGCAAGGCCCTGCT	5206
QY	3600	GTAATAGCTGGAGCCGTTTCAAAACGAGTTACTACCAACACCCCATTAACCAATACAT	3659
Db	5207	GTAACGCTGGAGCCGTTTCCAGATAGGTTACCTCTCACCCCATTAACCAATACAT	5266
QY	3660	CATGCGCATGATGTCCGCTACCTGGAGGTGTCAACAGACCTGGGTGCTGGTAGGCGG	3719
Db	5267	CATGCGCATGATGTCCGCTACCTGGAGGTGTCAACAGACCTGGGTGCTGGGTGGCGG	5326
QY	3720	AGTCCTTAGCAGCTCTGGCCGCGTATTGGCTGACAAACAGGCAAGCTGTGATTTGGGCAG	3779
Db	5327	AGTCCTTAGCAGCTCTGGCCGCGTATTGGCTGACAAACAGGCAAGCTGTGATTTGGGTAG	5386
QY	3780	GATCATCTTGCCGAGGCGCGGCACTCATTTCCGACAGGAGAGTCTTTACCCGGAGTT	3839
Db	5387	GATTATCTGTGCCGAGGCGCGGCACTTTGCCACAGGAGAGTCTTCTACAGAGATT	5446
QY	3840	CGATGAGATGGAAGAAGTGGCGCTCACACCTCCCTTACATCCGACAGGGAATGCAAGCTGC	3899
Db	5447	CGATGAATGGAAGAAGTGGCGCTCTGCACTCCCTTACATCGAGCGGAATGCAAGCTGC	5506
QY	3900	CGAACATTTCAACAGAGAGCAATGSGGTTGCTGCAACAGGCAACCAAGCAAGCGAGAGC	3959
Db	5507	CGAGCATTTCAAGCAGAAAGCGCTCGGGTTACTGCAAAACAGCCACCAACCAAGCGAGGC	5566
QY	3960	TGCTGCTCCCTGGTGSAAATCCAAATGTGGGAGACCCGCAAGGCTCTGGGGAGAGCAT	4019
Db	5567	TGCTGCTCCCTGGTGSAAATGTGGGAGACCCCTTGGAATTTCTGGGAGAGCAT	5626
QY	4020	GTGGAATTTCAATCAGCGGGATACAAATATTAGCAGGCTGTCCACTCTGCTGGCAACC	4079
Db	5627	GTGGAATTTCAATCAGCGGGATACAGTACTAGCAGGCTTATCCACTCTGCTGGGAACC	5686
QY	4080	CGCGATPACATCACTGATGAGCAATTCAAGGCTCTATACACACCGCGCTACACACGCAAA	4139
Db	5687	CGCATPACATCAATTGATGGAATTCAAGGCTTATACACACCGCGCTACACCCCAAG	5746
QY	4140	TACCTCTCTGTTTAAACATCTCGGGGGGATGTGGCGCGCCCAACTTGCCTCCAGCGC	4199
Db	5747	TACCTCTCTGTTTAAACATCTCGGGGGGATGTGGCGCGCCCAACTTGCCTCCAGCGC	5806
QY	4200	TGCTTCTGCTTGTGAGGCGCGGCACTCGGTGAGGCGGCTGTGGAGCATTAAGGCTTGG	4259
Db	5807	CGCTTGGCTTGTGAGGCGCGGCACTCGCGGTGGGCTGTGGGAGCATTAAGGCTTGG	5866
QY	4260	GAAAGTGCTTGTGATATTTTGGCAGGTTATGAGCAGGCGGTGGCAGCGCGCTGTGGC	4319
Db	5867	GAAAGTGCTTGTGACATTTCTGCGGGGTTATGAGCAGGAGTGTGGCGCGCGCTGTGGC	5926
QY	4320	CTTTAAGGCAATGAGCGCGGAGATGTCCCTACACGAGGACGTGGCTAACCTTACCTCCGC	4379
Db	5927	CTTTAAGGCAATGAGCGCGGAGATGTCCCTACACGAGGACGTGTAACTTACCTCCGC	5986
QY	4380	TATCTCTTCCCTGGCGCCTAAGTGTGGGGGTGTGTGGCAGCGATCTGTGTCGCCA	4439

Db	5987	CATCCTCTCTCTGCGCGCTTGGCTGGCTCGCGGGGCTCGATGTGTGAGCAATAACTGCTCTGACA	6046
Qy	4440	CGTGGGCCCAAGGGGAGGGGGGCTGTGCAGTGGATGAGACCGGGTGATAGGGTTCCGTTGGCG	4499
Db	6047	CGTGGGCTCGGGAGAGGGGGGCTGTGCGAGTGGATGAAACCGGCTGATAGCCTTCGCCCTGGCG	6106
Qy	4500	GGGTAAACCAAGCTCTCCCCACGACACTATGTCCCTGAGAGCGACGCTGCAGACGTGTAC	4559
Db	6107	GGGTAATCATGTTTCCCCACGCACTATGTGCTTGAGAGCGACGCGCGAGCGCGTGTATAC	6166
Qy	4560	TGAGATCTCTCTACTCTTACCATCACTACGTACGAGTGGTGAAGAGGTTTCAACAGTGAATCA	4619
Db	6167	TCGATCTCTCCAGCTTACCTACCTGCTCAAGTGGCTGTGAAGAGGCTTCACAGTGGATTTA	6226
Qy	4620	CGAGGACTGCTCCAGCGCATGCTCCGGGCTGTGGCTAAGAGATGTTTGGATTTGGATATG	4679
Db	6227	TGAAGACTGCTCCACACCGCTGTCCGGGTGTGGCTAAGGATGTTTGGAGCTGGATATG	6286
Qy	4680	CAGGGTGTACGTGATTTTCAGAGCTGGGCTTCAGTCCAGTCCAGTCCCTGCGCGCATTCGGCG	4739
Db	6287	CAGGGTGTAGCTGATTTTCAAGACTGGCTTCAGTCCAGTCCAGTCCCTGCGCGAGCTTACCTGG	6346
Qy	4740	AGTCCCTCTCTCTCATGCTCAACGTGGGTACAGAGGAGTGTGGCGGGGCGAGCGCATCAT	4799
Db	6347	AGTCCCTTTTCTCTGCTGCAACGGGGGTACAAAGGAGTCTGGCGGGGAGAGCGCATCAT	6406
Qy	4800	GCAACACACTGGCCATGTGGAGCAACAATACCGGAGCATGTGAATAAAAGTTCATAG	4859
Db	6407	GCAACACACTGCCCATGTGGAGCAGAGATCACCGGACATGTGAATAAAGCGTTTCATAG	6466
Qy	4860	GATCGTGGGGCTTAGACCTGTAGTACAGCTGSCATGGAACATTTCCTCATTAACGCTA	4919
Db	6467	GATCGTGGGGCTTAAGACCTGTGAGCAACATGGCAATTCCTCATTAACGCTA	6526
Qy	4920	CACGAGGGGCCCTGGACGCCCTCCCGGGGCCCAATATTATTCAGGGGCTGTGGCGGCT	4979
Db	6527	CACGAGGGGCCCTGGACGCCCTCTCCAGGCCCAATATTATTCAGGGGCTGTGGCGGCT	6586
Qy	4980	GGCTGCTGAGAGCTACGTGGAGGTTACGGGGGTGGGGATTTTCCATACGTACGGGAT	5039
Db	6587	GCGCGCTGAGAGTACGTGGAGGTACCGGGGTGGGGATTTTCCATACGTACGGGAT	6646
Qy	5040	GACCACGACAACGTAAAGTGCCTGTGACAGTTGCCGGCCCCGAATTTCTTACAGAAGT	5099
Db	6647	GACCACGACAACGTAAAGTGCCTGTGACAGTTGCCGGCTCTGATTTCTTCCGAGAGT	6706
Qy	5100	GGATGGGGTCCGTTGCACAGTACGCTTCACAGCTGCAAAACCCCTCTACGGGAGAGAGT	5159
Db	6707	GGAGCGAGTCCGGTTGCACAGTACGCTTCGGGCTGTGAGGCTCTCTTACGGGAGAGAGT	6766
Qy	5160	CACATTCCTGTGTGGGCTCAATCAATACCTGTTGGGTCAAGCTCCATGCGAGCCGA	5219
Db	6767	TACATTCACAGTGGGGCTCAACCAATACCTGTTGGGTCAAGCTCAATGCGAGCCGA	6826
Qy	5220	ACCGGAGCTAGAGTGTCTACTTCCATCTTCACCGAGCCCTCCACATTAAGCGGAGAGC	5279
Db	6827	ACCGGAGTGTAGAGTGTCTACTTCCATCTTCACCGAGCCCTCCACATTCACAGCAGAAC	6886
Qy	5280	GGCTAAACGTAGAGCTGAGCAGGAGGATCTCCGCCCTCTTGGAGCAGTCAAGTACCA	5339
Db	6887	GGCTAAAGGTAGGTGAGCAGGAGGATCTCCGCCCTCTTGGAGCAGTCAAGTACCA	6946
Qy	5340	GCTGTGTGGGCTCTCTTAAGGCAAAATGACACATACCGATGATGAGTCCCGGAGAGCTGA	5399
Db	6947	GTTGTCTGGGCTCTCTTGAAGCGACATGACATCCACCAATGTCTCTCGGAGCTGA	7006
Qy	5400	CCTCATGAGAGCAACCTCTGTGGCGCAGAGATGGCGGGGAACATCACCCCGCTGGA	5459
Db	7007	CCTCATGAGAGCAACCTCTGTGGCGCAGAGATGGCGGGGAACATCACCCCGCTGGA	7066
Qy	5460	GTCGAAATATAGTATATATTTGGACCTTTCAGCGCGCTCCAAAGCGAGAGATGA	5519

Db	7067	GTGGAGAACAAAGTGGTAGTCTCTGGACCTCTTCCACCCCGCTTGAGCGGAGAGAGATGA	7120
Qy	5520	GAGGAGATATCCGTTCCGGCGGAGATCTCTGGGAGGTCCAGGAATTTCCCTCAGCGAT	5579
Db	7127	GAGGAGATATCCGTTCCGGCGGAGATCTCTGGGAGGAATTCAGGAATTTCCCGCAGGAT	7186
Qy	5580	GCCCATTTGGGCAACCCCGSATTACAAACCTTCGACTGTTAAGTCTCTGGAAAGACCCGA	5639
Db	7187	GCCCATTTGGGCGCCCGGATTTCAACCTTCGACTGTTAAGTCTCTGGAAAGACCCGA	7246
Qy	5640	CTACGTCCTTCACAGTGGTATACAGCGTGTGTCATTGGCCGCTGGCAAGGCCCTTCGATACC	5699
Db	7247	CTACGTCCTTCGCGGTGGTGGACGGTGGCCGTTGGCACCTATCAAGGCCCTTCGATACC	7306
Qy	5700	ACCTCCACGGAGAGAGAGACGGTGTCTCTGTCCAGATCTACCGTGTCTTCTGCTTTGGC	5759
Db	7307	ACCTCCACGGAGAGAGAGAGCGGTTCTCTTAACAGATCTCTCCGTTCTTGTGGCTTAGC	7366
Qy	5760	GGAGCTCGCCACAAGACCTTGGGAGCTCCGATTCGATCGCGCGCTGCACAGCGCACGCGC	5819
Db	7367	GGAGCTCGCTACATAAGACCTTGGGAGCTTCGAGCTTCGATATGGCGCGTGCAGACGGCAGCGC	7426
Qy	5820	AACGGCTCTCTTGACCAAGCCCTTCGACGAGCGGCGACGCGGATCCGACGTTGAGTGGTA	5879
Db	7427	GACCGCCCTTCCTGACCAAGCCCTTCGACGAGCGGTGCAGAAAGATCCGACGTTGAGTGGTA	7486
Qy	5880	CTCCGTCATGCCCCCTTGAAGGGAGGCGGGGGATCCGAGTTCACGACGCGGTCTTG	5939
Db	7487	CTCCGTCATGCCCCCTTGAAGGGAGGACCGGGGACCCCGATCTCAGTAGAGGGTCTTG	7546
Qy	5940	GTCACCGTAAAGGAGGAGGCTAGTAGAGACGTCTGCTGCTCTCGATGTCTTACACATG	5999
Db	7547	GTCACCGTGAAGGAGGAGGCTAGTAGAGATGTGCTGCTCTCGTCAATGTCTTACACATG	7060
Qy	6000	GACAGGGGCCCTATATCACGSCCATGCGCTGGGAGAGAAACCAAGCTGCCCCATCAATGCACT	6059
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Qy	6120	CCTGGCGCAAGAAAGGTCACTTTGACAGACTGCGAGGTCTTGAGACACTATACCGGGA	6179
Db	7727	CCTGGCGGAGAAAGGTCACTTTGACAGACTGCGAGGTCTTGAGACACTATACCGGGA	7786
Qy	6180	CGTGCTCAAGAGATGAAGGCGAAAGGGTCCACAGTTAAGGCTAACTCTTACGCTGGA	6239
Db	7787	CGTGCTCAAGAGATGAAGGCGAAAGGGTCCACAGTTAAGGCTAACTCTTACGCTAGA	7846
Qy	6240	GAAGCCTGTAGCTGACGCCGCCACATTTGGCCAGATCTAAATTTGGCTATGGGCGAA	6299
Db	7847	GAAGCCTGTAGCTGACGCCGCCACATTTGGCCAGATCTAAATTTGGCTATGGGCGAA	7906
Qy	6300	GGAGCTCGGAACCTATTCACGAAAGGCGGTTACCACTCCGCTCGGTGTGAAGACTT	6359
Db	7907	GGAGCTCGGGAACCTATTCACGAAAGGCGGTTAAACCACTCCGCTGTGAAGACTT	7966
Qy	6360	GCTGGAAGACACTGAGACACCATTGACACACCACATCATGGCAAAAATGAGGTTTTCTG	6419
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Db	8147	GATGGGCTCTTCATACGATTTCCAATCTCTCTGGACACGCGGTGTGAGTCTCTGTGTGA	8206

QY	6600	TGCGTGAAGACGAGAAATGCCCTATGGGCTTCGCAATATGACACCGGCTTTTGACTC	6659
Db	8207	TACCTGGAATTCAGAAAGAAAAACCCCATGGGCTTTTCATATGACATCGCTTTTCGACTC	8266
QY	6660	AACGCTACAGAAATATGACATCCGTTGTAGAGATCAATCTCCAAATGTTGTGACTTGAC	6719
Db	8267	AACGCTACCGGAGACACATCCGTTGTAGAGATCAATTTACCAATGTTGTGACTTGAC	8326
QY	6720	CCCCGAAGCCAGACAGGCCATTAAGTTCGCTACACAGGCGGCTTTTACATCGGGGGCCCCCT	6779
Db	8327	CCCCGAAGCCAGACAGGCCATTAATAATCGCTACAGAGGCGGCTTTATATCGGGGGCTCTCT	8386
QY	6780	GACTAATTTAAAGGGGAGACATGCGGCTATGCGGCTGCCGCGGACGCGGTGACTGAC	6839
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QY	6840	GACCACTGCGGGTATATACCTCATATGTTACTTTGAAGGCGGCTGCGGCGCTTCGACGTGC	6899
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Db	8507	GAACTCTCCAGACATCGACGATGCTGCTGAGACGAGACGACCTGTGCTTATCTGTGAAG	8566
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Db	8627	CTTCGGCCCCCTCGGGGACCCCGGCCCAACCAAGATACGACTGGAAGCTGATATACATCATG	8686
QY	7080	CTCTCCCAATGTGTCACTGCGGCACAGATGATCTGSCAAAAGGTTGTACTATTCACCCG	7139
Db	8687	TTCTCCCAATGTGTGCTGCTCCCGACGATGATCAGCAAAAAGGTTGTACTATTCACCCG	8746
QY	7140	TGACCCACACACCCCCCTTGCGGGGGTGGTGGGAGAGAGTAAACACATCCACGTCAA	7199
Db	8747	TGATCCACACACCCCCCTTACGAGGGCTGCTGTGGAGAGCTAAGACACTCCAGTTAA	8806
QY	7200	TTCTCGGTAGGCAACATCATATGATGCGCCACCTTGTGGCAAGGATATGCTGAT	7259
Db	8807	CTCTCGGTAGGCAACATTTATATGATGCGCCACCTTGTGGCAAGGATATGCTGAT	8866
QY	7260	GACTCATTTCTTTCCATCTCTTAGCTAGGAGAACTTGA AAAAGCCCTGATTTGCA	7319
Db	8867	GACTCATTTCTTTCCATCTCTTAGCGGAGGAACTTGA AAAAGCCCTGACTGCA	8926
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QY	7500	TGTCCGGCTTGGGTACTGATGCCAGGGGGGAGAGGCTGACACTGAGCAATATACCTTT	7559
Db	9107	CTGTCCGGCTTGGGTACTGATGCCAGGAGGAGAGGCGCCACTTGTGGCAATATACCTTT	9166
QY	7560	CAACTGSGCAGTAAAGCAAGCTCAAACTCACTCCATATCCGGCTGCTCCCACTTGG	7619
Db	9167	CAACTGSGCAGTAAATAAACCAACTTAAACTCACTCCAAATCCGGCTGCTCCCGCTGGA	9226
QY	7620	TTTATTCACGCTGGTTCGTTGCTGGTTACACAGGGGGAGACATATATACAGCTGTGCG	7679
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RESULT 11
US-08-324-977-35
Sequence 35, Application US/08324977
Patent No. 5747339
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: MORE, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, Mcleland &
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 7863 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA from genomic RNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7863
FEATURE: misc.feature
NAME/KEY: misc.feature
LOCATION: 1..7863
OTHER INFORMATION: /note="sequence = 1500 - 9362 of
OTHER INFORMATION: SEQ ID NO: 1"
US-08-324-977-35
Query Match 64.8%; Score 5175.2; DB 1; Length 7863;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5468; Conservative 0; Mismatches 489; Indels 0; Gaps 0;
QY 1800 CATGGGCGCTATTACGGCTCTACTCCACAGACGCGAGGCTCTGGCTGCATCATC 1859
DB 1908 CCTCGCGCCCATATCAGCCCTACTCCACAGACGCGAGGCTCTGGCTGCATCATC 1967
QY 1860 TAGCCTACAGCGCGGAGACAGAACAGAGGAGGAGGAGTCCAGTGTCTCCACCGC 1919
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QY 1920 AACCAATCTTTCTGCGCACTGCGTCAATGCGTGTGTGTGACTGTCTATCATGTGC 1979
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QY 2100 CGGAGCTGGAGCTTACTTGTGACAGAGGAGTGGCGATGCTCCGCTGCGCGCG 2159
DB 2208 TGCGAGCTGAGCTTACTTGTGACAGAGGAGTGGCGATGCTCCGCTGCGCGCG 2267
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DB 2268 GGGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2327
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DB 2388 CAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2447
QY 2340 GCGGTCCCGCTGTACAGGACACTGTGCTCCGCGGAGGAGGAGGAGGAGGAGGAGGAG 2399
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QY 2400 GGGCCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2459
DB 2508 GGGCCTACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2567
QY 2460 AGCCCAAGGATATAGGTGCTTCTGTAACCGGCTCCGCGGAGGAGGAGGAGGAGGAGGAG 2519
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Db	2868	GCTGCCACCGCTTACGCTCTCGGGATCGGTACCGCTGCCACCAACATCTGAGAGGT	2927
Qy	2820	GGCTCTGCCAGCACTGGAGAAATCCCTTTATATGGCAAGCCATCCCATCGAGACAT	2879
Db	2928	GGCCCTGTCTTAATCTGGAGAGATCCCTCTTATATGGCAAGCCATCCCATTTAGAGCAT	2987
Qy	2880	CAAGGGGGGGGAGGACCTCATTTTCTGCCATTCCAGAAGAAATGTATGAGCTGCCGC	2939
Db	2988	CAGGGGGGGAAGGACATCTCATTTTCTGTATTCGAAGAAAGTGCAGCGCTGCCGC	3047
Qy	2940	GAACTGTCCGCTCGACTCAATTCCTGTACCAATTAACCGGGGCGCTGTATATCGT	2999
Db	3048	AAACCTGTACGGCTCGGAATCAACGCTGTGGCGATTACCGGGGGGCTGTATGTCCGT	3107
Qy	3000	CATACCACTAGCGGAGACGCTCATTTCTGTACCAACGGAGCGCTCTAATGAGCGGCTTAC	3059
Db	3108	CATACCACTATGTGGAGACGCTCTGTCTGTGGCAACAGAGCGTCTGATGAGAGGCTATAC	3167
Qy	3060	CGGCGATTGCACTCACTGATGCACTGTGCAATATGTGTACCCAGACAGTCTGACTTAC	3119
Db	3168	GGGCGACTTTGACTCACTGATGCACTGTGCAATATGTGTACCCAGACAGTCTGACTTAC	3227
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Qy	3180	GCAGCGGCGAGGACGAGGACTGTAGAGGGCAGAGATGGGCAATTTACAGTTTGTACTCAG	3239
Db	3288	GCAGCGGCGGAGTGTGACTGTGACAGGGGTAGAGAGGCACTCTACAGTTTGTACTCAG	3347
Qy	3240	AAAGAGGCGCTCGGGCAATGTTCAATTCCTCGTCTGTGTGAGTGTCTATGACGGGGGTG	3299
Db	3348	AAAGAGGCGCTCGGGCAATGTTCAATTCCTCGTCTGTGTGAGTGTCTATGAGCGGGGTG	3407
Qy	3300	TGCTTGTACAGAGCTCAAGCGCCGCGGCGAGACCTAGTTAGTTGCGGGCTTACCTAAAC	3359
Db	3408	TGCTTGTACAGAGCTCAAGCGCCGCGGCGAGACCTGTAGTTGCGGGCTTACCTAAAC	3467
Qy	3360	ACCAAGGTTGCCCGCTCTGCCAGAGACCATCTGTGAGTCTGTGGAGAGAGCTTTTACAGGCT	3419
Db	3468	ACCAAGGTTGCCCGCTCTGCCAGAGACCATCTGTGAGTCTGTGGAGAGAGCTTTTACAGGCT	3527
Qy	3420	CACCCACATAGAGCGCCATTTCTTGTGTCCAGATTAAGCAAGGAGAGCAACTTCCCTA	3479
Db	3528	CACCCACATAGAGTGCACACTTCTGTGTCCAGACCAAGCAAGGAGAGCAACTTCCCTA	3587
Qy	3480	CCGTGTAGCATACAGGCTTACGCTGCTGCCAGAGGCTCAGGCTCCACTTCCATCTGTGGGA	3539
Db	3588	CCGTGTAGCATACAGGCTTACGCTGCTGCCAGAGGCTCAGGCTCCACTTCCATCTGTGGGA	3647
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Db	3708	GTAACAGCTGGAGAGCGGCTCAAGAAATGAGGTACCCCTACCCCATATACCAATACAT	3767
Qy	3660	CATGGATCATAGTGGCTGTGACGTGGAGAGTGTACAGAGACCTGGGTCTGTATGGGG	3719
Db	3768	CATGGATCATAGTGGCTGTGACGTGGAGAGTGTACATGACACCTGGGTCTGTATGGGG	3827
Qy	3720	AGCTCAGAGGCTGTGGCGGGATTGTGCTGTGCAACAGGAGCGCTGTATTTGTGGCGAG	3779

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Db	4308	CGCTTGGCTTTCGTTGGGCGCGCGGCATCGCGGTGCTGGGAGCATAGGCTTGG	4367
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Qy	4560	TGCAATCCCTCTAGCTTACCATCATCAGCACTGCTGAGAGGGCTTACCAAGTGGATCAAA	4617
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Page 37

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US-08-384-616-35
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Patent No. 5847101
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Ieao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Ieao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, Mcleland &
ADDRESS: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

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COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
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FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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FILING DATE: 02-OCT-1991
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
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FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 687-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA from genomic RNA
FEATURE:
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US-08-384-616-35

Query Match          64.8%; Score 5175.2; DB 2; Length 7863;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5466; Conservative 0; Mismatches 488; Indels 0; Gaps 0.

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QY 1860 TAGCCTACAGCGCGGAGAGGAGAACAGTAGGTGAGGGGAGGTCCAGGTGCTCCACCAG 1919
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RESULT 13
US-08-904-686A-35
Sequence 35: Application US/08904686A
Patent No. 5998130
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroko
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mclelland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0357
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:
LENGTH: 7863 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA from genomic RNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7863
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..7863
OTHER INFORMATION: /note= "sequence - 1500 - 9362 of
OTHER INFORMATION: SEQ ID NO: 1"
US-08-904-686A-35

Query Match 64.8%; Score 5175.2; DB 2; Length 7863;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 5468; Conservative 0; Mismatches 488; Indels 0; Gaps 0;
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RESULT 14
US-09-315-850-35
Sequence 35, Application US/09115850
Patent No. 621/872
GENERAL INFORMATION:
APPLICANT: OKAYAMA, HIROTO
APPLICANT: FUKE, ISAO
APPLICANT: MORI, CHISATO
APPLICANT: TAKAMIZAWA, AKAHISA
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McJeland &
ADDRESS: Naughton
STREET: 1725 K St. N.W. Suite 1000

Mon Jun 2 08:44:25 2003

us-10-005-469-4.rn1

Page 44

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315.850
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-AUG-1997
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
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APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Mcleland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 9007036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 7863 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA from genomic RNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7863
NAME/KEY: misc_feature
LOCATION: 1..7863
OTHER INFORMATION: /note= "sequence = 1500 - 9362 of
OTHER INFORMATION: SEQ ID NO: 1"
US-09-315-850-35

Query Match 64.88: Score 5175.2: DB 4: Length 7863;
Best Local Similarity 91.88: Pred. No. 0;
Matches 5468: Conservative 0; Mismatches 488: Indels 0; Gaps 0;

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Db	3228	CTTGATATCCCACTTCATCATTGAAACGACACACGCTGTGCTTCACACGCACTGTCCGGCTTC	3287
QY	3180	GCACCGGCGAGGAGGACTGGTAGGGGGAGGATGGGGCACTTACAGGTTTGTGACTCCAGG	3239
Db	3288	GCACCGGCGGGGAGGACTGGTAGGGGGTAGAGAGGCACTTACAGGTTTGTGACTCCGGG	3347
QY	3240	AGAACGGCCCTCGGGGCAATGTCGATTCCTCGGTTCTGTGCGATGTCTATACGCGGGCTG	3299
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QY	3300	TGCTGGTAGAGCTACACGCGCCGCGAGACCTCATTTAGTGTGGGGCTTACCTAAACAC	3359
Db	3408	TGCTGGTAGAGACTCACCCCGCGAGACCTCGGTTAGTTGGGGGCTTACCTGAACAC	3467
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Db	6108	GACAGAGCCCTTGTATCAGCGCCATCGCTGGGAGAGAAAGCAACCTCCCATAAAGCGTT	6167
QY	6060	GAGCAACTCTTGTCTCGCTACCAACAATTGTGCTATGCTAAACAATCTCGAGCGCAG	6119
Db	6168	GAGCAACTCTTGTCTCGGCGCCACCAATACATGTTTATGCCAACAACTCTCGAGCGCAG	6227
QY	6120	CCTGGGGAGAAAGAGTCACTTGTGACACAGTGCAGGTCCTGTGAGAGACACTACCGGA	6179
Db	6228	CCTGGGGAGAAAGAGTCACTTGTGACAGCTGTGACAGTCTGTGAGAGACACTACCGGA	6287
QY	6180	CGTGTCTAAGAGATGAAGGGAAGGCGTCCACAGTTAAAGCTTAACTCTATCCGTGA	6239
Db	6288	CGTGTCTAAGAGATGAAGGGAAGGCGTCCACAGTTAAAGCTTAACTCTATCCGTGA	6347
QY	6240	GGAGACGTGTAAAGTGAAGCGCCCAACATTCGGGCAAGTCTAAATTTGGCTATGGGGCAAA	6299
Db	6348	GGAGACGTGTCAAGCTGAAGCGCCCAACATTCGGGCAAAATCCAAATTTGGCTATGGGGCAAA	6407
QY	6300	GGAGCTCCGGAACCTATCCAGCAAGGCGGTTAACACATCCGCTCCGTGTGAAGGACTT	6355

Db	6408	GGAGTTCGGAGACCTTCTCCAGCAAGGCCGTTTACCACATCTCCACTCCGTTGGAGAGACTT	6467
Qy	6360	CGCTGGAGAGACGTGAGAGCAACCAATTGACACACCACATCAATGGCAAAAATGAGATTTCTCG	6419
Db	6468	GCTTGGAAGACACTGTGACACCAATTGTACACCCACCATCATGTGGCAAAAAATGAGGTTTTCTCG	6527
Qy	6420	CGTTCACACCGAGAGAAAGGGGGGCGCGCAAGCCAGCTGCGCTTATCGTATTTCCAGATTTGGG	6479
Db	6528	TGTCACACCGAGAGAAAGAGGAGCGCGTTAAGCCACCGCGCTTATCGTATTTCCAGATTTGGG	6587
Qy	6480	GGTTCGTGTGTGGAGAAATGGCCCTTTACGTATGGTCTGACCCCTCCACCCCTCCAGGCGGT	6539
Db	6588	AGTCGGTGTATGGAGAAAGTGGCCCTCTATGTATGGTCTCCACCCCTCTCCAGGCTGT	6647
Qy	6540	GATGGGCTCTTCATACGAGATTCCAAATCTCTCTGTGACACGCGGTGTGAGTTCTGTGTAA	6599
Db	6648	GATGGGCTCTTCATACGAGATTCCAGTACTCTCTGTGGCGAGCAGTCGAGTTCTGTGTAA	6707
Qy	6600	TGCGTGGAAAGCGGAAGAAATGGCCCTTATGGGCTTCGATATGACACCCGATGTTTGGATTC	6659
Db	6708	TACCTGGAAATCAAGAAAAACCCCATGGGCTTTTATATGACACTCGCTGTTTGACATC	6787
Qy	6660	AACGCTCACTAGATGACATCCGTTGTGAGAGTCAATCTACCAATGTTGTGACTTGGC	6719
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Qy	6720	CCCCGAGCCAGACAGGCCCATTAAGATGTCGCTACAGAGCGGCTTTACATCGGGGGGCCCCCT	6779
Db	6828	CCCCGAGCCAGACAGGCCCATTAATAATGCTCACAGAGCGGCTTTATATCGGGGGGCTCT	6887
Qy	6780	GACTAATTTCTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGCGAGCGGTGTACTGAC	6839
Db	6888	GACTAATTTCTAAAGGCGAGAACTGCGGCTATCCCGGTGCGCGCGAGCGGTGTACTGAC	6947
Qy	6840	GACACAGTCGGGTATTAATCCCTACATGTTTCTTGAAGGCGCGGTGTCGACGTGCG	6899
Db	6948	GACTAGCTGCGGTATACACCTCTCATATGTTACTTGAAGGCGCTCTGACGCTGTGAGCTGCG	7007
Qy	6900	GAACTCCAGGACTGTCACGATGCTCGTATGCGGAGACGACTTGTCTTATCTGTGAAG	6959
Db	7008	GAACTCCAGGACTGTCACGATGCTCGTATGCGGAGAGACGACTGTGTATGTGTGAAG	7067
Qy	6960	CGCGGGGACCCCAAGAGGACGAGGAGACCTTACGCGGCTTACGAGAGGCTATGACTAGATA	7019
Db	7068	CGCGGGGACCCCAAGAGGACGCGGAGACCTTACGAGCTTACGAGAGGCTATGACTAGATA	7127
Qy	7020	CTTTCGCCCCCTTGSGGACCCGCCAAACCAAGATACGACTTGGAGTTATATACATCATG	7079
Db	7128	CTTCGCCCCCTTGSGGAGCCCGCCCCCAACCAAGATACGACTTGGAGCTATATACATCATG	7187
Qy	7080	CTTCGTCCAATGTGTACGTGCGGCGACGTGATGTGGCAAAAGGTTACTATATCTACCGG	7139
Db	7188	CTTCGTCCAATGTGTGCGGTGCGGACGATGATGAGCAAAAGGTTACTATATCTACCGG	7247
Qy	7140	TGACCCGACACCCCCCTTGCGGCGGCTGCGTGTGGAGACAGCTAGACACACTCCAGTCAA	7199
Db	7248	TGATCCGACACCCCCCTTAGACGCGGTGTGTGGAGACAGCTAGACACACTCCAGTTTAA	7307
Qy	7200	TTCCTGCGGTAGGACAACATCATATGTATGGCCGACCTTGTGGCGAAGGATGATCTGAT	7259
Db	7308	CTTCGCGGTAGGACAACATTAATATGTATGTGGCCGACCTTGTGGCGAAGGATGATCTGAT	7367
Qy	7260	GACTCATTTTCTTTCATCTCTTACGTACGAGAAACAATTGAAAAAGCCCTAGATTGTCA	7319
Db	7368	GACTCATTTTCTTTCATCTCTTACGTACGAGAGCAACATGTGAAAAAGCCCTGACTGCCA	7427
Qy	7320	GATCTACCGGGGCGTTACTCATATGAGCCACTTGAACCTTACCTCAGATCATTTCAAGACT	7379
Db	7428	GATCTACCGGGGCGTTACTCATATGAGCCACTTGAACCTTACCTCAGATCATTTGAACACT	7487
Qy	7380	CGATGGCCTTAGGCCATTTTACATCCCATATTTACTCTCCAGAGTGAATCAATAGGCTGGC	7439
Db	7488	CGATGGCCTTAGGCCATTTTACTCTCCATATGTACTCTCCAGGTGAATCAATAGGCTGGC	7547

QY 7440 TTGATGCTCAGAGAACTGGGGTACCGCCCTTGGAGCTGTGAGACATCGGGCCAGAG 7499
DB 7548 TTATGCTCAGAGAACTGGGGTACCGCCCTTGGAGCTGTGAGACATCGGGCCAGAG 7607
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RESULT 15
US-08-324-977-13
Sequence 13, Application US/08324977
Patent No. 5747339
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &
ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990

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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA from genomic RNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..9030
OTHER INFORMATION: /note: "sequence = 333 - 9362 of
OTHER INFORMATION: SEQ ID NO: 1"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..9030
US-08-324-977-13

Query Match 64.8%; Score 5175.2; DB 1; Length 9030;
Best Local Similarity 91.8%; Pred No. 0;
Matches 5468; Conservative 0; Mismatches 488; Indels 0; Gaps 0;

QY 1800 CATGGCGCTATTATCGGCTTACTCCACAGACGCGAGGCTTACTTGCCTGCATCATAC 1859
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QY 1860 TAGCCTCAGAGCGCGGACAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1929
DB 3135 TAGCCTCAGAGCGCGGACAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3194
QY 1920 AACACATCTTCTCTGCGGACGCTGCTCAATGCGCTGCTGCTGCTGCTGCTGCTGCTG 1979
DB 3195 AACACATCTTCTCTGCGGACGCTGCTCAATGCGCTGCTGCTGCTGCTGCTGCTGCTG 3254
QY 1980 CGGCTCAAGACCTTCCGCGCCCAAGGCGCCCAATCACCACCAATGACCAATGACCA 2039
DB 3255 TGCTCTAAGACCTTCCGCGCCCAAGGCGCCCAATCACCACCAATGACCAATGACCA 3314
QY 2040 CCAAGACCTTCTCTGCGGACGCTGCTCAATGCGCTGCTGCTGCTGCTGCTGCTGCTG 2099
DB 3315 CCAAGACCTTCTCTGCGGACGCTGCTCAATGCGCTGCTGCTGCTGCTGCTGCTGCTG 3374
QY 2100 CGGAGCTCGGACCTTACTTGTGTCAAGAGCATGCTGCTGCTGCTGCTGCTGCTGCTG 2159
DB 3375 TGAGAGCTCGGACCTTACTTGTGTCAAGAGCATGCTGCTGCTGCTGCTGCTGCTGCTG 3434
QY 2160 GGGGAG 2219
DB 3435 GGGGAG 3494
QY 2220 GGGGAG 2279
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QY 2280 CACCGAG 2339
DB 3555 CACCGAG 3614
QY 2340 GCGGTCCCGCTCTTCAAG 2399
DB 3615 GCGGTCCCGCTCTTCAAG 3674
QY 2400 GGGCCTCTACAGCGCCCTCTGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2459
DB 3675 GGGCCTCTACAGCGCCCTCTGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3734

Db	4815	TCAAATGTGGAAGTGTTCATACGGCTGAACCTTACGCTGCACGGGCCAACACCCCTTCT	4874
Qy	3600	GTATAGGCTGGAGACCCGTTTAAACAGAGTTACTACACACACCCCATTAACCAATATAC	3659
Db	4875	GTACAGGCTGGAGACCCCTCCAGATAGAGGTACACCCACCCACCCCATTAACCAATATAC	4934
Qy	3660	CATGGCATGATGTCGGCTACCTGAGAGGTCGTACAGACACTGGAGTCGTATGGCGG	3719
Db	4935	CATGGCATGATGTCGGCTACCTGAGAGGTCGTACTACACCTGGAGTCGTATGGCGG	4994
Qy	3720	AGTCCTAGACACTTGGCCCGCATTTGCCGACACAGGACAGCTGTACTTGTGGCAG	3779
Db	4995	AGTCCTTAGACACTTGGCCCGCATTTGCCGACACAGGACAGCTGTACTTGTGGCAG	5054
Qy	3780	GATCATCTTGGCGGAGGGCGGCGCATTCCTCCGACAGGAGTCCTTACCGGAGTT	3859
Db	5055	GATTATCTTGTCCGGAGGCCCGGCATTTGTTCCGACAGGAGCTTCTTACAGAGATT	5114
Qy	3840	CGATGAGATGGAAGAGTGGCCCTTCACACCTCCCTTACATCGAACAGGATATGCACTGC	3899
Db	5115	CGATGAATGGAAGAGTGGCCCTTCACACCTCCCTTACATCGAGAGGATATGCACTGC	5174
Qy	3900	CGAACATTCACAAAGAAAGCAATCGGGTGTCTGCAACAGCACCAACACAGCGAGGC	3959
Db	5175	CGAGCAATTCAGAGAAAGACCGCTCGGGTTACTGCAAAAGCCACCAACAAAGCGAGGC	5234
Qy	3960	TGCTGCTCCGCTGTGGAATTCAGATGTCGGGACCTTCGAACCTTCTGTGGCGAACAAT	4019
Db	5235	TGCTGCTCCGCTGTGGAATTCAGATGTCGGGACCTTCGAACCTTCTGTGGCGAACAAT	5294
Qy	4020	GTGGAATTCATACGCGGATACAAATATTAGACAGGCTTGCATCTGTGCTGTGGCAACC	4079
Db	5295	GTGGAATTCATACGCGGATACAGTACTAGACAGGCTTATCCATCTGTGCTGTGGCAACC	5354
Qy	4080	CGCATATGATCATGTGATGCGATTACAGGCTTATACACAGCCGGCTTACACCCACAC	4139
Db	5355	CGCATATGATCATGTGATGCGATTACAGGCTTATACACAGCCGGCTTACACCCACAAAG	5414
Qy	4140	TACCTCTCTGTTTACATCCTGAGGGGATGGTGGCGCGCCCAACTGTCCTCCACGCG	4199
Db	5415	TACCTCTCTGTTTACATCCTGAGGGGATGGTGGCGCGCCCAACTGTCCTCCACGCG	5474
Qy	4200	TGCTTCTGCTTTCGTATAGGCGCGGCATCGCTGAGCGGCTGTTGGAGATAGGCGCTTG	4259
Db	5475	CGCTTCCGCTTTCGTATAGGCGCGGCATCGCGGTGGGCTGTTGGAGATATGGCGCTTG	5534
Qy	4260	GAAGTGTCTGTGATATTTTGTGGAGTTATGAGCAGAGGGGTGGCGAGCGCGCTGTGGC	4319
Db	5535	GAAGTGTCTGTGATATTTTGTGGAGTTATGAGCAGAGGGGTGGCGAGCGCGCTGTGGC	5594
Qy	4320	CTTTAAGGTCATGAGCGCGAGATGCCCTCACCGAGGACGTGGTAACCTACTCCGCG	4379
Db	5595	CTTTAAGGTCATGAGCGCGAGATGCCCTCACCGAGGACGTGGTAACCTACTCCGCG	5654
Qy	4380	TATCCTCTCCCATGGCCCGCTAGTGTGCGGGGTGTGTGCGCAGCGATACTGCTGCGCA	4439
Db	5655	CATCCTCTCTCCCATGGCCCGCTAGTGTGCGGGGTGTGTGCGCAGCGATACTGCTGCGCA	5714
Qy	4440	CGTGGGCCAGGGAGGGGGGTGTGCATGTGATGAACCGGGTATATGCGTGTGCTTCGG	4499
Db	5715	CGTGGGTCCGGAGAGGGGGGTGTGCATGTGATGAACCGGGTATATGCGTGTGCTTCGG	5774
Qy	4500	GGGTACACAGCTCTCCCGCAGCACTATGTGCTGAGAGCAGCGCTGACGACAGTGCAC	4559
Db	5775	GGGTATCATATGTTTCCCGCAGCACTATGTGCTGAGAGCAGCGCGCGCGCTGTAC	5834
Qy	4560	TGAGATCTCTCTAGTGTACATCACTACGTCGTGAAGAGCTTCAACAGTGTGATTA	4619
Db	5835	TGAGATCTCTCTCAGCCTTACATCACTACGTCGTGGAAGAGCTTCAACAGTGTGATTA	5894
Qy	4620	CGAGGATGCTCCAGCCCATGCTCCGGCTGTGGCTAAGAGATGTTTGGATTGATATG	4679

Db	5895	TGAAGACTGCTCCACACCGCTTCGCGGCTGCGCTAAAGATGTTTGGGACTGGATATG	5994
Qy	4680	CACGGTGTGACATGATTTCAAGACGTGGCTCCAGTCCAAAGCTCTGCGCGATTTGCCGGG	4739
Db	5995	CACGGTGTGACTGACTTCAAGACGTGGGCTCCAGTCCAAAGCTCTGCGCGAGTACTGGG	6014
Qy	4740	AGTCCCTTCTCTCTCATGTCAACGTGGGTACAAGGAGAGCTGGCGGGCGAGCGGATCAT	4799
Db	6015	AGTCCCTTCTTCTCTGTCGTCGACACGCGGGTACAAGGAGAGCTGGCGGGGAGAGGATCAT	6074
Qy	4800	GCAACACACCTGGCCATGTGGAGCACAGATCAACCGACATGTGAAAAAAGTTTCATAG	4859
Db	6075	GCAACACACCTGGCCCATGTGGAGCACAGATCAACCGACATGTGAAAAAAGGTTTCATAG	6134
Qy	4860	GATGCTGGGGCTTAGACCTCTGTAGTAAACAGTGGCATGGAACATTTCCCATTTAAGGCTA	4919
Db	6135	GATGCTGGGGCTTAGAGCCGTAGACCAACAGTGGCATGGAACATTTCCCATTAACGCATA	6194
Qy	4920	CACACAGGCGCCCTGCACGCGCTTCCCGGGGCCAAATTAATCTAGGGCTTGGCGGCT	4979
Db	6135	CACACAGGCGCCCTGCACACCCCTTCCAGCGCCAAACTTTCTAAGGGGCTTGGCGGCT	6254
Qy	4980	GCTTGTGAGGAGTACGTGAGGTTACGCGGCTGGGGGATTTTCCACTACGTACGGGAT	5039
Db	6255	GGCCGTGAGGAGTACGTGAGGTTACGCGGCTGGGGGATTTTCCACTACGTACCGGAT	6314
Qy	5040	GACACATGACAAAGTAAAGTGGCGGTACAGTTCGCGGCGCCGAAATTTTACACAGAGT	5099
Db	6315	GACACATGACAAAGTAAAGTGGCGGTACAGTTCGCGGCGCCGAAATTTTCTCGAGAGT	6374
Qy	5100	GGATGGGGTGGCGTTTGACAGAGTACGCTCCAGCGTCCAAACCCCTCTACGGGAGAGGT	5155
Db	6375	GGACGAGATGGCGTTTGACAGAGTACGCTCCGCGGTCCAGGCTCTCTACGGGAGAGGT	6433
Qy	5160	CACATTCCTGGTCCGGGCTCAATCAATACGTGGGTCAACAGCTCCCATGGAGCCGA	5214
Db	6435	TACATTCAGGTTGGGCTCAACCAATACGTGGGTCAACAGTCCCATGGAGCCGA	6494
Qy	5220	ACCGGACGTACAGTGTCACTTCCATGCTACACGACCCCTCCACATTACGGCGAGAC	5275
Db	6435	ACCGGATGTACAGTGTCACTTCCATGCTACACGACCCCTCCACATCAACAGCAAGAAC	6554
Qy	5280	GGCTAAGCGTGAAGCTGGCCAGAGGATTCCTCCCTCTTGGCCAGCTCATACAGTACGA	5333
Db	6555	GGCTAAGCGTGAAGTGGCCAGAGGATTCCTCCCTCTTGGCCAGCTCTTACAGTACGA	6614
Qy	5340	GCTGTCTCGGCTTCTGGAAGCAATGACATGACATCCCGTATGACTCCCGGAGCTGA	5399
Db	6615	GTTGTCTCGGCTTCTTGAAGGCGAATGACATGACATCCCGTATGCTCTCCGAGGCTGA	6674
Qy	5400	CCTCATGAGGCAACCTCTGTGTGGCGGACAGAGATGGCGGACATCACCCGCTGGA	5455
Db	6675	CCTCATGAGGCAACCTCTGTGTGGCGGACAGAGATGGCGGACATCACCCGCTGGA	6733
Qy	5460	GTCAGAAAATAGAGTAAATTTTGGACTCTTGAGCCGCTCCAGACGGAGAGATGA	5514
Db	6735	GTCGAGAACAAAGTGGTAAAGTCTCTGAGACTCTTTGACCCGCTTCGAGCGAGAGATGA	6794
Qy	5520	GAGGGAAGTATCCGTTCCGCGGGAGATCTGCGGAGGTCCAGGAATTTCCCTGAGGAT	5577
Db	6795	GAGGGAAGTATCCGTTCCGCGGGAGATCTGCGGAAATTCAGAAAGTTCCTCCGACGAT	6855
Qy	5580	GGCCATATGGGACGCCCGGATTAACACCCGCCACTTGAAGTCCGGAAGGAGACCGGA	5633
Db	6855	GGCCATATGGGCGGCCCGGATTAACACCCCTTCACTTTAGAGTCTCGAAGGAGACCGGA	6914
Qy	5640	CTACGCTCCCTCAGTGTACACAGGATGTCAATTGACCCCTGACAGGCGCCCTCCGATACC	5699
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Qy	5700	ACCTCAGAGGAGAGAGAGAGGTTGTCTGTACAGATCTACAGTGTCTTCTGCGCTTGGC	5755
Db	6975	ACCTCAGAGGAGAGAGAGAGGTTGTCTTAACAGAGTCTCGGTGTCTTCTCCTTACG	7033

QY	5760	GGAGCTGGCCACAAAGACCTTGGGAGAGCTCCGATCTGCTGGCGGCTGACAGCGGACGAGGC	581
Db	7035	GGAGCTGGCTACTAGAGACCTTGGGAGCTCCGATATATGGCGCTGACAGCGGACGAGGC	7034
QY	5820	AACGGCCCTCTCTACACGAGCCCTCCGACGACGCGCGACGCGGAGTCCGACGTTGACTCGTA	5879
Db	7095	GACCGCCCTTCTGACCAAGCCCTCCGACGACGAGTGCAGAGATCCGACGTTGAACTCGTA	7154
QY	5880	CTCTCCATGCCCCCTTTAGAGGGGAGCCGGGGATCCCGATCTCAGAGAGGGCTCTG	5939
Db	7155	CTCTCCATGCCCCCTTTAGAGGGGAGCCGGGGACCCCGATCTCAGAGAGGGCTCTG	7214
QY	5940	GCTTACCGTAAGCAGGAGAGGCTAGTGAAGCAGTCTGCTGCTAGATGCTCTACACATG	5999
Db	7215	GCTTACCGTGAAGCAGGAGAGTGAATGATGAGATGCTGCTGCTGCTCAATGCTCTACACATG	7274
QY	6000	GACAGGCGCCCTGATTCACAGCCATGCGGTGGGAGGAAACCAAGCTGCCCATCAATGACCT	6059
Db	7275	GACAGGCGCCCTTGAATCACAGCCATGCGGTGGGAGGAAACCAAGCTGCCCATCAAGCGCT	7334
QY	6060	GAGCACTCTTGGTCCGTCACGACCACTTGTGTATGCTACACATCTCGACGCGCAAG	6119
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QY	6120	CCTGGGGAAGAAAGGTCACCTTGAACACTGACAGGTCGTGGAGGACCACTACCGGGA	6179
Db	7395	CCTGGGGAAGAAAGGTCACCTTGAACACTGACAGGTCGTGGAGGACCACTACCGGGA	7454
QY	6180	CGTGCTCAAGAGATGAAGAGCGGAGCGGTCCACAGTTAAAGCTTAACTTATCCGTGA	6233
Db	7455	CGTGCTCAAGAGATGAAGAGCGGAGCGGTCCACAGTTAAAGCTTAACTTATCCGTGA	7514
QY	6240	GGAAACCTGTAAAGCTGACAGCCGCCACACTTGGGCGAGTCTAAATTTGGCTATAGGGCAAA	6299
Db	7515	GGAAACCTGTCAAGCTGACAGCCGCCACACTTGGGCGAATTCCAATTTGGCTATAGGGCAAA	7577
QY	6300	GGAGCTCCGGAACCTATCCAGCAAGGCGGTTAAACACATCGCTCCGTGTGAAGACTT	6355
Db	7575	GGAGCTCCGGAACCTATCCAGCAAGGCGGTTAAACACATCGCTCCGTGTGAAGACTT	7634
QY	6360	GCTGGAAGCACTGAGCACCAATTGACACACACATCATGGCAAAATGAGATTCTTG	6419
Db	7635	GCTGGAAGCACTGAGCACCAATTGACACACACATCATGGCAAAATGAGATTCTTG	7694
QY	6420	CGTCCACACAGAAGAGGGGGCGCGCAAGCAAGCACTCGCTTATGCTATTCACGATTTGGG	6477
Db	7695	TGTCACACACAGAAGAGGGCGCTTAAAGCACGCCGCTTATGCTATTCACGATTTGGG	7755
QY	6480	GGTTCGTGTGTGCGGAAGAAATGAGCCCTTGAAGATGTGTTCACACCTCCCTCAGAGCCT	6533
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QY	6600	TGCTGTGAAGGAGGAAGTAATCCCTATGAGGTTTGCATATGACACCCGCTGTTTGACTC	6653
Db	7875	TACCTGTGAAGTAAGAAAGAAACCCCATAGGCTTTTCTATGACACCTGCTGTTTGACTC	7933
QY	6660	AACGCTACTGGAATGACATCCGTTGAGAGACTCAATACCAATGTTGTACTTGGC	6711
Db	7935	AACGCTACCGGAAGACGACATCCGTTGAGAGACTCAATTAACCAATGTTGTACTTGGC	7999
QY	6720	CCCCGAGGCAACAGGCGCATAAAGTGCCTACAGACCGGCTTTACATGGGGGCCCTCT	6777
Db	7995	CCCCGAGGCAACAGGCGCATTAATGCTCTACGAGCGGCTTTATATGGGGGCTCTCT	8055
QY	6780	GACTAATTTAAAGGCGAGAACTGGGCTATCGCCGCTGCCGCGGAGGCGTACTGAC	6833
Db	8055	GACTAATTTAAAGGCGAGAACTGGGCTATCGCCGCTGCCGCGGAGGCGGCTGCTGAC	8111

Mon Jun 2 08:44:25 2003

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QY	6840	GACACAGCTGGGGTAATAAACCTCAACATGTTACTGAAAGCCGCTGCGGCTGTGAGCTGC	6899
Db	8115	GACTAGCTGGGTAACACACCTCACTAGTTACTGTAAGGCTCTCTCAGCTGTGAGCTGC	8174
QY	6900	GAAGCTCCAGAGCTGACAGTACTGTATGCGGAGACGACCTTGCTATCTGTGAAG	6959
Db	8175	GAAGCTCCAGAGCTGACAGTACTGTATGCGGAGACGACCTTGCTATCTGTGAAG	8234
QY	6960	CGCGGSAACCCAAAGAGAGAGAGGCGAGGCTTACAGGCTCTTCACAGAGCTATGATATATA	7019
Db	8235	CGCGGSAACCCAAAGAGAGAGAGGCGAGGCTTACAGGCTCTTCACAGGAGGTATGATATAGTA	8294
QY	7020	CTCGACCCCGCTGGGGAGCCGCGCAAAACACAAATACACTGTGAGTTGATACATCATG	7079
Db	8295	CTCGACCCCGCTGGGGAGCCGCGCAAAACACAAATACACTGTGAGTTGATACATCATG	8354
QY	7080	CTCTCTCCAATGTGTCAAGTGGCGAGCATGTACATCTGGCAAAAAGGTTACTCTCACCAG	7139
Db	8355	TTCTCCCAATGTGTGGGTGCGCCACGATCATCAGCAAAAGGGTTACTCTCACCAG	8414
QY	7140	TGACCCACACACCCCTCTTGCGGGGCTCGTGGGAGACAGCTAGACACTCCAGTCAA	7199
Db	8415	TGATCCACACACCCCTTACACAGGCGCTCGTGGGAGAGCTAGACACTCCAGTTAA	8474
QY	7200	TTCTTGGCTAGGCACATCATATATATGCGCCACCTTGTGGGCAAGATGATCCGAT	7259
Db	8475	CTCTTGGCTAGGCACATTTATATGATGCGCCACTTGTGGGCAAGAGATGATTCGAT	8534
QY	7260	GACTCATTTCTTCATCCTCTTACTAGGAGACACTTGAAAAGCCCTAGATTGCA	7319
Db	8535	GACTCATTTCTTCATCCTCTTACTAGGAGACACTTGAAAAGCCCTGAGCTGCA	8594
QY	7320	GATCTAGGSGGCTGTTACTCATCTGAAGCACTTGACACTTACTCTAGATCATTCACAGCT	7379
Db	8595	GATCTAGGSGGCTGTTACTCATCTGAAGCACTTGACACTTACTCTAGATCATTCGAAGCT	8654
QY	7380	CCATGGCTTGAAGCATTTTCACCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGC	7439
Db	8655	CCATGGCTTGAAGCATTTTCACCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGC	8714
QY	7440	TTTCATGCTCAGGAAACTTGGGGTACCGCCCTTGCGAGTCTGAGAGCATGGGCCAAG	7499
Db	8715	TTTCATGCTCAGGAAACTTGGGGTACCGCCCTTGCGAGTCTGAGAGCATGGGCCAAGAG	8774
QY	7500	TGTCCGSGCTAGGCTACTGTCGCCAGGGGGGAGGGCTGCGACATTGGGCAATGACTCTT	7559
Db	8775	CGTCCGSGCTAGGCTACTGTCGCCAGGGAGGAGGAGGGCGGCACATTGGGCAATGACTCTT	8834
QY	7560	CAACTGGGCACTAAGAGCAAGCTCAACTACTCCATCTCCGGCTGCGTCCCACTGGA	7619
Db	8835	CAACTGGGCACTAAGAGCAAGCTCAACTACTCCAAATCCGGGCTGCGTCCCGCTGGA	8894
QY	7620	TTTATTCACAGCGTGTGCTGTGCTGTACAGCGGGGGAGACATTTATCAAGGCTCTGCG	7699
Db	8895	CTTGTCCGAGTGTGCTGTGCTGTACAGCGGGGGAGACATTTATCAAGGCTCTGCG	8954
QY	7680	TGCCCCAGCCCGCTGGTTCATGTGCTGCTACTCTACTTCTGTGAGGGTATGACATCTA	7739
Db	8955	TGCCGAGCCCGCTGGTTCATGTGCTGCTACTCTACTTCTGTGAGGGTATGAGCATCTA	9014
QY	7740	TCTACTCCCAACGA 7755	
Db	9015	CTGCTCTCCCAACGA 9030	

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